GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 27 Seconds
(without alignments)
1340.918 Million cell updates/sec

Title: US-10-690-991-2
Perfect score: 2542
Sequence: 1 MAYGTHSHGLFKKLGIPGPT.....PVVLKVESRDGTVSGAHHHH 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2501	98.4	508	4	US-09-949-016-7092	Sequence 7092, Ap
2	2501	98.4	508	4	US-09-949-016-8562	Sequence 8562, Ap
3	2494	98.1	503	4	US-09-144-367-2	Sequence 2, Appli
4	2233	87.8	508	4	US-09-949-016-8561	Sequence 8561, Ap
5	2142.5	84.3	502	4	US-09-949-016-5992	Sequence 5992, Ap
6	2142.5	84.3	507	4	US-09-949-016-7091	Sequence 7091, Ap
7	1957	77.0	503	4	US-09-583-447A-2	Sequence 2, Appli
8	1946.5	76.6	504	1	US-08-457-274A-25	Sequence 25, Appl
9	1946.5	76.6	504	4	US-09-583-447A-4	Sequence 4, Appli
10	1946.5	76.6	504	5	PCT-US95-05758-25	Sequence 25, Appl
11	1620	63.7	420	4	US-09-583-447A-6	Sequence 6, Appli
12	840.5	33.1	554	4	US-09-949-016-11161	Sequence 11161, A
13	840.5	33.1	554	4	US-09-949-016-11162	Sequence 11162, A
14	802	31.5	250	4	US-09-583-447A-8	Sequence 8, Appli
15	721.5	28.4	529	4	US-09-270-767-46468	Sequence 46468, A
16	671	26.4	507	1	US-08-457-274A-22	Sequence 22, Appl
17	671	26.4	507	5	PCT-US95-05758-22	Sequence 22, Appl
18	643	25.3	526	1	US-08-298-426-4	Sequence 4, Appli
19	630	24.8	498	1	US-08-457-274A-24	Sequence 24, Appl
20	630	24.8	498	5	PCT-US95-05758-24	Sequence 24, Appl
21	621.5	24.4	507	1	US-08-457-274A-23	Sequence 23, Appl
22	621.5	24.4	507	5	PCT-US95-05758-23	Sequence 23, Appl
23	591	23.2	517	1	US-08-457-274A-2	Sequence 2, Appli
24	591	23.2	517	5	PCT-US95-05758-2	Sequence 2, Appli
25	588	23.1	517	1	US-08-457-274A-28	Sequence 28, Appl
26	588	23.1	517	5	PCT-US95-05758-28	Sequence 28, Appl
27	569.5	22.4	1023	4	US-09-270-767-43827	Sequence 43827, A
28	518.5	20.4	372	4	US-09-270-767-33357	Sequence 33357, A
29	518.5	20.4	372	4	US-09-270-767-48574	Sequence 48574, A
30	428.5	16.9	510	4	US-09-852-067-2	Sequence 2, Appli
31	426	16.8	524	4	US-09-976-594-533	Sequence 533, App
32	425	16.7	512	4	US-09-270-767-45399	Sequence 45399, A
33	423.5	16.7	245	4	US-09-270-767-43855	Sequence 43855, A
34	416.5	16.4	520	4	US-09-949-016-6003	Sequence 6003, Ap
35	416.5	16.4	527	4	US-09-949-016-10078	Sequence 10078, A
36	416	16.4	520	4	US-09-527-073-2	Sequence 2, Appli
37	415.5	16.3	576	3	US-08-948-564-16	Sequence 16, Appl
38	410.5	16.1	489	4	US-09-852-067-4	Sequence 4, Appli
39	409	16.1	508	3	US-09-111-730-2	Sequence 2, Appli
40	409	16.1	508	4	US-09-949-016-5994	Sequence 5994, Ap
41	409	16.1	523	4	US-09-949-016-10466	Sequence 10466, A
42	401	15.8	500	4	US-09-949-016-7973	Sequence 7973, Ap
43	400	15.7	476	1	US-08-313-075A-30	Sequence 30, Appl
44	394	15.5	557	3	US-09-518-386B-1	Sequence 1, Appli
45	394	15.5	557	3	US-09-518-386B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-7092
; Sequence 7092, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7092
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7092

Query Match 98.4%; Score 2501; DB 4; Length 508;
Best Local Similarity 100.0%; Pred. No. 3.4e-244;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         30 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 89

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 149

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 209

Qy        183 ENTKKLLRFDFLDPFFLSITVPPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 ENTKKLLRFDFLDPFFLSITVPPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 269

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
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Db        330 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 389

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
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Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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RESULT 2
US-09-949-016-8562
; Sequence 8562, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8562
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8562

  Query Match             98.4%;  Score 2501;  DB 4;  Length 508;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-244;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         30 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 89

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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Db         90 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 149

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 209

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
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Db        210 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 269

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Db        270 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 329

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
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Db        330 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 389

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
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Db        390 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 449

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        450 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 508


RESULT 3
US-09-144-367-2
; Sequence 2, Application US/09144367
; Patent No. 6432639
; GENERAL INFORMATION:
;  APPLICANT: Lichter, Jay
;  APPLICANT:  Guido, Marco
;  TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
;  FILE REFERENCE: SEQ-12P
;  CURRENT APPLICATION NUMBER: US/09/144,367
;  CURRENT FILING DATE:  1998-08-31
;  PRIOR APPLICATION NUMBER: 60/058,612
;  PRIOR FILING DATE: 1997-09-10
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-09-144-367-2

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  Best Local Similarity   99.8%;  Pred. No. 1.7e-243;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
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Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
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Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 4
US-09-949-016-8561
; Sequence 8561, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
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;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8561
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8561

  Query Match             87.8%;  Score 2233;  DB 4;  Length 508;
  Best Local Similarity   88.7%;  Pred. No. 4.6e-217;
  Matches  425;  Conservative   27;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         30 YGTRTHGLFKKLGIPGPTPLPFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPMLAI 89

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||:|||||||||||:|||||||||||||||||
Db         90 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 149

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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Db        150 MVPIIAQYGDVLVRNLRREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFV 209

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
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Db        210 ENTKKLLRFNPLDPFVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKET 269

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Db        270 QKHRVDFLQLMIDSQNSKDSETHKALSDLELMAQSIIFIFAGYETTSSVLSFIIYELATH 329

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
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Db        330 PDVQQKVQKEIDTVLPNKAPPTYDTVLQLEYLDMVVNETLRLFPVAMRLERVCKKDVEIN 389

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        390 GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 449

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        450 MRFALVNMKLALVRVLQNFSFKPCKETQIPLKLRFGGLLLTEKPIVLKAESRDETVSGA 508


RESULT 5
US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5992
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-5992

  Query Match             84.3%;  Score 2142.5;  DB 4;  Length 502;
  Best Local Similarity   84.1%;  Pred. No. 6.5e-208;
  Matches  402;  Conservative   37;  Mismatches   38;  Indels    1;  Gaps    1;

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Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
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Db        205 ESTKKFLKFGFLDPLFLSIILFPFLTPVFEALNVSLFPKDTINFLSKSVNRMKKSRLNDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||:|||||||||||||| |:|||||||||||||||:|:|||| ||||||||
Db        325 PDVQQKLQKEIDAVLPNKAPPTYDAVVQMEYLDMVVNETLRLFPVAIRLERTCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| :|:||:|||| |||||||||:| ||||||| ||:|||||||||:|||||||
Db        385 GVFIPKGSMVVIPTYALHHDPKYWTEPEEPRPERFSKK-KDSIDPYIYTPFGTGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||||||||||||||||||||||||||||||    ||||||||:||||:|||||:||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLDTQGLLQPEKPIVLKVDSRDGTLSG 501


RESULT 6
US-09-949-016-7091
; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7091
;   LENGTH: 507
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7091

  Query Match             84.3%;  Score 2142.5;  DB 4;  Length 507;
  Best Local Similarity   84.1%;  Pred. No. 6.6e-208;
  Matches  402;  Conservative   37;  Mismatches   38;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| :|||||:|||||||||| |||:||| :|   || ||:|||||:|| |:|| |||||
Db         30 YGTRTHGLFKRLGIPGPTPLPLLGNVLSYRQGLWKFDTECYKKYGKMWGTYEGQLPVLAI 89

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||:|:|||||||||||||  ||||||||||:||||||||:|||||||||||||||||
Db         90 TDPDVIRTVLVKECYSVFTNRRSLGPVGFMKSAISLAEDEEWKRIRSLLSPTFTSGKLKE 149
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Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||||||||||||||||||| ||||||||:|||||||||| ||||||||||||||||||
Db        150 MFPIIAQYGDVLVRNLRREAEKGKPVTLKDIFGAYSMDVITGTSFGVNIDSLNNPQDPFV 209

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |:||| |:| |||| |||| :|||| |: | ||: :||::  ||| ||| |||:||| |
Db        210 ESTKKFLKFGFLDPLFLSIILFPFLTPVFEALNVSLFPKDTINFLSKSVNRMKKSRLNDK 269

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||:|||||||||||||||||||||||| ||||||||||||||||||| :||||||
Db        270 QKHRLDFLQLMIDSQNSKETESHKALSDLELAAQSIIFIFAGYETTSSVLSFTLYELATH 329

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||:|||||||||||||| |:|||||||||||||||:|:|||| ||||||||
Db        330 PDVQQKLQKEIDAVLPNKAPPTYDAVVQMEYLDMVVNETLRLFPVAIRLERTCKKDVEIN 389

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| :|:||:|||| |||||||||:| ||||||| ||:||||||||||:|||||||
Db        390 GVFIPKGSMVVIPTYALHHDPKYWTEPEEFRPERFSKK-KDSIDPYIYTPFGTGPRNCIG 448

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||||||||||||||||||||||||||||    |||||||:||||:|||||:||
Db        449 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLDTQGLLQPEKPIVLKVDSRDGTLSG 506
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RESULT 7
US-09-583-447A-2
; Sequence 2, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOWSKI, Leszek
; APPLICANT: GELLNER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-447A-2

Query Match 77.0%; Score 1957; DB 4; Length 503;
Best Local Similarity 76.2%; Pred. No. 3.9e-189;
Matches 364; Conservative 51; Mismatches 63; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               |||||||||||||||||: | ||:||:|||:| ||||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| |||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | |||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||| ||| ::|||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:|||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||| |:|||:|| |||||||||||||||||    :||||||:||||  |||  ||
Db        445 MRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 502
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RESULT 8
US-08-457-274A-25
; Sequence 25, Application US/08457274A
; Patent No. 5734086
; GENERAL INFORMATION:
; APPLICANT: Scott, Jeffrey G.
; APPLICANT: Tomita, Takashi
; TITLE OF INVENTION: Cytochrome P450lpr Gene and Its Uses
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: P.O. Box 1051, Clinton Square
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,274A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/240 (D-1519)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1304
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rat
; STRAIN:
; DEVELOPMENTAL STAGE: Adult
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
US-08-457-274A-25

Query Match 76.6%; Score 1946.5; DB 1; Length 504;
Best Local Similarity 74.0%; Pred. No. 4.5e-188;
Matches 355; Conservative 62; Mismatches 62; Indels 1; Gaps 1;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              :|| :|||||| |||| |||| | :|:|: |   ||:|||||||:|| :||| |: ||
Db         25 FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               || :||| |||||:||||||| ||||| |  |:|:|:|||||| |:||||||||:|||
Db         85 TDTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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                 | ||| ||||:||: |::|||||||||:| ||||||||||||||||||:||||||:||||
Db        145 MPPIIEQYGDILVKYLKQEAETGKPVTMKKVFGAYSMDVITSTSFGVNVDSLNNPKDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              | ||||||||| || ||||: :|||| || |:||||:||::   | :| | ||||:||:
Db        205 EKTKKLLRFDFFDPLFLSVVLFPPLTPIYEMLNICMFPKDSIEFFKKFVYRMKETRLDSV 264

Qy        243 QKHRVDFLQLMIDSQN-SKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              ||||||||||:::  | ||: ||| ||||:|: |||||||||||| ||| |||::: |||
Db        265 QKHRVDFLQLMMNAHNDSKDKESHTALSDMEITAQSIIFIFAGYEPTSSTLSFVLHSLAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              ||| |:|||||||  |||||||||||::|||||||:||||||:||  ||||||||||||
Db        325 HPDTQKKLQEEIDRALPNKAPPTYDTVMEMEYLDMVLNETLRLYPIGNRLERVCKKDVEI 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              ||:|:||| |||||||||||||::| |||:| |||||||:|| :||||:| |||:||||||
Db        385 NGVFMPKGSVVMIPSYALHRDPQHWPEPEEFRPERFSKENKGSIDPYVYLPFGNGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||| :|||||||:||||||||||  ||||| ||::|||  ||  ::|:
Db        445 GMRFALMNMKLALTKVLQNFSFQPCKETQIPLKLSRQGLLQPTKPIILKVVPRDEIITGS 504


RESULT 9
US-09-583-447A-4
; Sequence 4, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
;  APPLICANT: WOJNOWSKI, Leszek
;  APPLICANT:  GELLNER, Klaus
;  APPLICANT:  EISELT, Regina
;  TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
;  TITLE OF INVENTION:  (CYP3A) GENE FAMILY: CYP3AX
;  FILE REFERENCE: 310115.401
;  CURRENT APPLICATION NUMBER: US/09/583,447A
;  CURRENT FILING DATE:  2000-05-30
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 504
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-583-447A-4

  Query Match            76.6%;  Score 1946.5;  DB 4;  Length 504;
  Best Local Similarity  76.0%;  Pred. No. 4.5e-188;
  Matches  364;  Conservative   51;  Mismatches   63;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||: | ||:||:|||:| |||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | |||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||| ||| ::|||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPE-RFSKKNKDNIDPYIYTPFGSGPRNCI 421
              |:|||||: ||:| |||| |||||||||| || |||||||:|| | | |||:||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPESRFSKKNKDSIDLYRYIPFGAGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||| |:|||:|| ||||||||||||||||||    :||||||:||||  |||  ||
Db        445 GMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 503


RESULT 10
PCT-US95-05758-25
; Sequence 25, Application PC/TUS9505758
;  GENERAL INFORMATION:
;    APPLICANT:  Cornell Research Foundation, Inc.
;    TITLE OF INVENTION:  Cytochrome P450lpr Gene and Its
;    TITLE OF INVENTION:  Uses
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle
;      STREET:  P.O. Box 1051, Clinton Square
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05758
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/241 (D-1519)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1304
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  504 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Rat
;      STRAIN:  Unknown
;      DEVELOPMENTAL STAGE:  Adult
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:  Unknown
PCT-US95-05758-25

  Query Match            76.6%;  Score 1946.5;  DB 5;  Length 504;
  Best Local Similarity  74.0%;  Pred. No. 4.5e-188;
  Matches  355;  Conservative   62;  Mismatches   62;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              :|| :|||||| ||||| |||| | :|:|: |   ||:|||||||:|| :||| |: ||
Db         25 FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              || :||| ||||||:||||||| ||||| |   |:|:|:|||||| |:||||||||:|||
Db         85 TDTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||| ||||:||: |::|||||||||:| ||||||||||||||||||:||||||:||||
Db        145 MFPIIEQYGDILVKYLKQEAETGKPVTMKKVFGAYSMDVITSTSFGVNVDSLNNPKDPFV 204
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Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
Db        205 EKTKKLLRFDFFDPLFLSVVLFPFLTPIYEMLNICMFPKDSIEPFKKFVYRMKETRLDSV 264

Qy        243 QKHRVDFLQLMIDSQN-SKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
Db        265 QKHRVDFLQLMMNAHNDSKDKESHTALSDMEITAQSIIFIFAGYEPTSSTLSFVLHSLAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
Db        325 HPDTQKKLQEEIDRALPNKAPPTYDTVMEMEYLDMVLNETLRLYPIGNRLERVCKKDVEI 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
Db        385 NGVFMPKGSVVMIPSYALHRDPQHWPEPEEFRPERFSKENKGSIDPYVYLPFGNGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
Db        445 GMRFALMNMKLALTKVLQNFSFQPCKETQIPLKLSRQGLLQPTKPIILKVVPRDEIITGS 504
```

RESULT 11
US-09-583-447A-6
; Sequence 6, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOWSKI, Leszek
; APPLICANT: GELLNER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-447A-6

Query Match 63.7%; Score 1620; DB 4; Length 420;
Best Local Similarity 75.9%; Pred. No. 3.8e-155;
Matches 299; Conservative 45; Mismatches 50; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPER 396
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPER 418
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RESULT 12
US-09-949-016-11161
; Sequence 11161, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11161
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11161

Query Match 33.1%; Score 840.5; DB 4; Length 554;
Best Local Similarity 35.9%; Pred. No. 4.6e-76;
Matches 183; Conservative 100; Mismatches 182; Indels 45; Gaps 10;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
Db         52 YSTSAFSRLEKLGLRHPKPSPFIGNLTFFRQGFWESQMELRKLYGPLCGYYLGRRMFIVI 111

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISI--AEDEEWKRLRSLLSPTFTSGKL 120
Db        112 SEPDMIKQVLV-ENFSNFTNRMASG-LEFKSVADSVLFLRDKRWEEVRGALMSAFSPEKL 169

Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
Db        170 NEMVPLISQACDLLLAHLKRYAESGDAFDIQRCYCNYTTDVVASVAFGTPVDSWQAPEDP 229

Qy        181 FVENTKKLLRFDFLDPFFLSITVFP-FLIPILEVLNICVFPR----EVTNFLRKSVKRMK 235
Db        230 FVKHCKRFFEFCIPRPILVLLLSFPSIMVPLARIL-----PNKNRDELNGFFNKLIRNVI 284

Qy        236 ESR-LEDTQKHRVDFLQLMIDSQNS----------------------KETESH------ 265
Db        285 ALRDQQAAEERRRDFLQMVLDARHSASPMGVQDFDIVRDVFSSTGCKPNPSRQHQPSPMA 344

Qy        266 KALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATHPDVQQKLQEEIDAVLPNKAPPTY 325
Db        345 RPLTVDEIVGQAFIFLIAGYEIITNTLSFATYLLATNPDCQEKLLREVDVFKEKHMAPEF 404

Qy        326 DTVLQ-MEYLDMVVNETLRLFPIAMRLERVCKKDVEINGMFIPKGVVVMIPSYALHRDPK 384
Db        405 CSLEEGLPYLDMVIAETLRMYPPAFRFTREAAQDCEVLGQRIPAGAVLEMAVGALHHDPE 464

Qy        385 YWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIGMRFALMNMKLALIRVLQNFSFK 444
Db        465 HWPSPETFNPERFTAEARQQHRPFTYLPFGAGPRSCLGVRLGLLEVKLTLLHVLHKFRFQ 524

Qy        445 PCKETQIPLKLSLGGLLQPEKPVVLKVESR 474
Db        525 ACPETQVPLQLESKSALGPKNGVYIKIVSR 554
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RESULT 13
US-09-949-016-11162
; Sequence 11162, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11162
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11162

Query Match 33.1%; Score 840.5; DB 4; Length 554;
Best Local Similarity 35.9%; Pred. No. 4.6e-76;
Matches 183; Conservative 100; Mismatches 182; Indels 45; Gaps 10;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         52 YSTSAFSRLEKLGLRHPKPSPFIGNLTFFRQGFWESQMELRKLYGPLCGYYLGRRMFIVI 111

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISI--AEDEEWKRLRSLLSPTFTSGKL 120
              ::|||| ||| | :| ||||   | : |   | |:    |: |: :|  |   |:  ||
Db        112 SEPDMIKQVLV-ENFSNFTNRMASG-LEFKSVADSVLFLRDKRWEEVRGALMSAFSPEKL 169

Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
              ||||:|:|  |:|: :|:| ||:|    ::  :  |: ||: | :||  :||    |:||
Db        170 NEMVPLISQACDLLLAHLKRYAESGDAFDIQRCYCNYTTDVVASVAFGTPVDSWQAPEDP 229

Qy        181 FVENTKKLLRFDFLDPPFLSITVFP-FLIPILEVLNICVFPR----EVTNFLRKSVKRMK 235
              ||:: |:   |    |  : :  ||  ::|:  :|     |     |:  |  | :: :
Db        230 FVKHCKRFFEFCIPRPILVLLLSFPSIMVPLARIL-----PNKNRDELNGFFNKLIRNVI 284

Qy        236 ESR-LEDTQKHRVDFLQLMIDSQNS----------------------KETESH------ 265
              |  :  :: | ||||:::|:::|                       :  |
Db        285 ALRDQQAAEERRRDFLQMVLDARHSASPMGVQDFDIVRDVFSSTGCKPNPSRQHQPSPMA 344

Qy        266 KALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATHPDVQQKLQEEIDAVLPNKAPPTY 325
              : |:  |:| |: ||: ||||  :: |||  | |||:|| |:||  |:|        | :
Db        345 RPLTVDEIVGQAFIFLIAGYEIITNTLSFATYLLATNPDCQEKLLREVDVFKEKHMAPEF 404

Qy        326 DTVLQ-MEYLDMVVNETLRLFPIAMRLERVCKKDVEINGMFIPKGVVVMIPSYALHRDPK 384
              :: : : |||||: ||||:|| | |   :| |: | || | |: :   ||| ||:
Db        405 CSLEEGLPYLDMVIAETLRMYPPAFRFTREAAQDCEVLGQRIPAGAVLEMAVGALHHDPE 464

Qy        385 YWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIGMRFALMNMKLALIRVLQNFSFK 444
              :|  || | ||||: : :    |: | |||:|||:|:|:|  |: :|| |: ||  | |:
Db        465 HWPSPETFNPERFTAEARQQHRPFTYLPFGAGPRSCLGVRLGLLEVKLTLLHVLHKFRFQ 524

Qy        445 PCKETQIPLKLSLGGLLQPEKPVVLKVESR 474
              | |||:||:|     | |:  | :|: ||
Db        525 ACPETQVPLQLESKSALGPKNGVYIKIVSR 554

RESULT 14
US-09-583-447A-8
; Sequence 8, Application US/09583447A
; Patent No. 6645745
; GENERAL INFORMATION:
; APPLICANT: WOJNOWSKI, Leszek
; APPLICANT: GELLNER, Klaus
; APPLICANT: EISELT, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401
; CURRENT APPLICATION NUMBER: US/09/583,447A
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-447A-8

Query Match 31.5%; Score 802; DB 4; Length 250;
Best Local Similarity 73.9%; Pred. No. 1e-72;
Matches 147; Conservative 23; Mismatches 29; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||: | ||:||:|||:| ||||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPPFLSI 201
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Db        205 KNMKKLLKLDFLDPFLLLI 223
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RESULT 15
US-09-270-767-46468
; Sequence 46468, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46468
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46468

Query Match 28.4%; Score 721.5; DB 4; Length 529;
Best Local Similarity 33.9%; Pred. No. 4.8e-64;
Matches 172; Conservative 111; Mismatches 181; Indels 43; Gaps 16;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILS-YHKGFCMFDMEC--HKKYG--KVWGFYDGQQ 57
              : : ::  ||  ||     |: : ||:   : :   |||: |  : | |  | :| :: :|
Db         32 WASANNDFFKDRGIAYEKPVLYFGNMAGMFLRKRAMFDIVCDLYTKGGSKKPFGIFEQRQ 91

Qy         58 PVLAITDPDMIKTVLVKECYSVFTNRR----------PFGPVGFMKSAISIAEDEEWKRL 107
              |:| : |||:|| : :|: :  | | |          |       |::    |  || :
Db         92 PLLMVRDPDLIKQITIKD-FDHFINHRNVFATSSDDDPHDMSNLFGSSLFSMRDARWKDM 150

Qy        108 RSLLSPTFTSGKLKEMVPIIAQYGDVLVRNLRREAE--TGKPVTLKDVFGAYSMDVITST 165
              || ||| ||  |:::|  :: |     |  |:::        : :||    :: ||| ||
Db        151 RSTLSPAFTGSKMRQMFQLMNQVAKEAVDCLKQDDSRVQENELDMKDYCTRFTNDVIAST 210

Qy        166 SFGVNIDSLNNPQDPFVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTN 225
              :||: ::|  : :: | :  |||  | ||    :   :|  |  : ::| : :| |: |
Db        211 AFGLQVNSFKDRENTFYQMGKKLTTFTFLQS--MKFMLFFALKGLNKILKVELFDRKSTQ 268

Qy        226 -FLRKSVKRMKESRLEDTQKH---RVDFLQLMIDSQNSKETESHKA-----LSDLELVAQ 276
               |:|  :  ||        |:|   | | : ::::::   :||  ||       || ::|||
Db        269 YFVRLVLDAMKY-----RQEHNIVRPDMINMLMEARGIIQTEKTKASAVREWSDRDIVAQ 323

Qy        277 SIIFIFAGYETTSSVLSFIMYELATHPDVQQKLQEEIDAV---LPNKAPPTYDTVLQMEY 333
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                :| |||:||:: :: |  :||  : ||||:| ||:  |   |  |   ||: :: |:|
Db        324 CFVFFFAGFETSAVLMCFTAHELMENQDVQQRLYEEVQQVDQDLEGK-ELTYEAIMGMKY 382

Qy        334 LDMVVNETLRLFPIAMRLERVCKKDV--EING--MFIPKGVVVMIPSYALHRDPKYWTEP 389
              || |||| || :| |: ::| | ||:  :::|  : : || |: :|:   ||||||:  |
Db        383 LDQVVNEVLRKWPAAIAVDRECNKDITFDVDGQKVEVKKGDVIWLPTCGFHRDPKYFENP 442

Qy        390 EKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIGMRFALMNMKLALIRVLQNFSFKPCKET 449
               || ||||| :||::| |: | ||| | ||||| ||||:  |  :  :|::: | | |::
Db        443 MKFDPERFSDENKESIQPFTYFPFGLGQRNCIGSRFALLEAKAVIYYLLKDYRFAPAKKS 502

Qy        450 QIPLKLSLGGL-LQPEKPVVLKVESRD 475
               |||:|   |  | |:    :|:  |:
Db        503 CIPLELITSGFQLSPKGGFWIKLVQRN 529


Search completed: July  8, 2005, 14:14:55
Job time : 32 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 175 Seconds
(without alignments)
1419.191 Million cell updates/sec

Title: US-10-690-991-2
Perfect score: 2542
Sequence: 1 MAYGTHSHGLFKKLGIPGPT.....PVVLKVESRDGTVSGAHHHH 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2501	98.4	503	2	Q86SK3	Q86sk3 homo sapien
2	2494	98.1	502	1	CP34_HUMAN	P08684 homo sapien
3	2449.5	96.4	503	1	CP33_HUMAN	P05184 homo sapien
4	2372	93.3	503	1	CP38_MACFA	P33268 macaca fasc
5	2372	93.3	503	2	Q6VP01	Q6vp01 macaca mula
6	2366	93.1	503	2	Q6PSM4	Q6psm4 macaca mula
7	2283	89.8	503	1	CP3L_CALJA	O18993 callithrix
8	2233	87.8	503	1	CP37_HUMAN	P24462 homo sapien
9	2215	87.1	535	2	Q9H241	Q9h241 homo sapien
10	2212	87.0	430	2	Q7Z448	Q7z448 homo sapien
11	2142.5	84.3	502	1	CP35_HUMAN	P20815 homo sapien
12	2112	83.1	503	2	Q6GUQ3	Q6guq3 macaca mula
13	2077	81.7	503	1	CP3C_CANFA	P24463 canis famil
14	2025	79.7	503	2	Q8HZK1	Q8hzk1 canis famil
15	2000	78.7	503	1	CP39_RAT	P51538 rattus norv
16	1997	78.6	503	1	CP3O_SHEEP	Q29496 ovis aries
17	1989	78.2	501	1	CP36_RABIT	P11707 oryctolagus
18	1983	78.0	503	1	CP3T_PIG	P79401 sus scrofa
19	1979	77.9	503	2	O97689	O97689 sus scrofa
20	1961	77.1	503	1	CP3D_MOUSE	Q64464 mus musculu
21	1957	77.0	503	1	C343_HUMAN	Q9hb55 homo sapien
22	1952	76.8	503	2	Q95L35	Q95l35 sus scrofa
23	1946.5	76.6	504	1	CP31_RAT	P04800 rattus norv
24	1935.5	76.1	504	1	CP3B_MOUSE	Q64459 mus musculu
25	1929	75.9	503	2	Q76N65	Q76n65 sus scrofa
26	1918.5	75.5	504	1	CP32_RAT	P05183 rattus norv
27	1906.5	75.0	504	1	C341_MOUSE	Q9jma7 mus musculu
28	1904.5	74.9	502	2	Q06884	Q06884 rattus norv
29	1902.5	74.8	502	2	Q6LEQ2	Q6leq2 rattus norv
30	1885	74.2	497	2	Q8CJF2	Q8cjf2 rattus norv
31	1885	74.2	507	1	CP3S_BOVIN	P79102 bos taurus
32	1884	74.1	503	1	CP3E_CAVPO	Q64417 cavia porce
33	1878.5	73.9	504	1	CP3G_MOUSE	Q64481 mus musculu
34	1877	73.8	503	1	CP3P_MOUSE	O09158 mus musculu
35	1876	73.8	503	2	Q9QXK4	Q9qxk4 mus musculu
36	1857	73.1	503	1	CP3F_CAVPO	Q64406 cavia porce
37	1849.5	72.8	504	2	Q9EQW4	Q9eqw4 mus musculu
38	1846	72.6	503	1	CP3H_CAVPO	Q64409 cavia porce
39	1835	72.2	501	1	CP3V_MESAU	O70537 mesocricetu
40	1802	70.9	497	1	CP3I_RAT	Q64581 rattus norv
41	1788	70.3	503	1	CP3A_MESAU	Q64148 mesocricetu
42	1696	66.7	353	2	Q86SK2	Q86sk2 homo sapien
43	1596	62.8	508	2	Q9PU44	Q9pu44 gallus gall
44	1560.5	61.4	504	2	Q6PA11	Q6pa11 xenopus lae
45	1550	61.0	496	1	C330_FUNHE	Q9pve8 fundulus he

ALIGNMENTS

RESULT 1
Q86SK3
ID Q86SK3 PRELIMINARY; PRT; 503 AA.
AC Q86SK3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome P450.
GN Name=CYP3A43/CYP3A4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing.";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ563375; CAD91343.1; -.
DR HSSP; P14779; 1JPZ.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004497; F:monooxygenase activity; IDA.
DR GO; GO:0050649; F:testosterone 6-beta-hydroxylase activity; IDA.
DR GO; GO:0006805; P:xenobiotic metabolism; TAS.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR InterPro; IPR008072; EP450_CYP3A.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR01689; EP450IICYP3A.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 503 AA; 57394 MW; 4141F95B28B34A6E CRC64;

Query Match 98.4%; Score 2501; DB 2; Length 503
Best Local Similarity 100.0%; Pred. No. 3.8e-174;
Matches 479; Conservative 0; Mismatches 0; Indels

Qy 3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKV
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Db 25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYG

Qy 63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKR
|||||||||||||||||||||||||||||||||||||||||||||||
Db 85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEW

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Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
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Db        205 ENTKKLLRFDFLDPFFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503
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RESULT 2
CP34_HUMAN
ID   CP34_HUMAN   STANDARD;   PRT;   502 AA.
AC   P08684; Q16757; Q9UK50;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A4 (EC 1.14.13.67) (Quinine 3-monooxygenase)
DE   (CYPIIIA4) (Nifedipine oxidase) (NF-25) (P450-PCN1).
GN   Name=CYP3A4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88195781; PubMed=3267210;
RA   Gonzalez F.J., Schmid B.J., Umeno M., McBride O.W., Hardwick J.P.,
RA   Meyer U.A., Gelboin H.V., Idle J.R.;
RT   "Human P450PCN1: sequence, chromosome localization, and direct
RT   evidence through cDNA expression that P450PCN1 is nifedipine
RT   oxidase.";
RL   DNA 7:79-86(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87041402; PubMed=3464943;
RA   Beaune P.H., Umbenhauer D.R., Bork R.W., Lloyd R.S., Guengerich F.P.;
RT   "Isolation and sequence determination of a cDNA clone related to human
RT   cytochrome P-450 nifedipine oxidase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:8064-8068(1986).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89108438; PubMed=2563251;
RA   Spurr N.K., Gough A.C., Stevenson K., Wolf C.R.;
RT   "The human cytochrome P450 CYP3 locus: assignment to chromosome 7q22-
RT   qter.";
RL   Hum. Genet. 81:171-174(1989).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=89093163; PubMed=2463251;
RA   Bork R.W., Muto T., Beaune P.H., Srivastava P.K., Lloyd R.S.,
RA   Guengerich F.P.;
RT   "Characterization of mRNA species related to human liver cytochrome P-
RT   450 nifedipine oxidase and the regulation of catalytic activity.";
RL   J. Biol. Chem. 264:910-919(1989).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=99256082; PubMed=10322772;
RA   Chen Q., Wu J., Yu Y.;
RT   "Establishment of transgenic cell line CHL-3A4 and its metabolic
RT   activation.";
RL   Zhonghua Yu Fang Yi Xue Za Zhi 32:281-284(1998).
RN   [6]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21163842; PubMed=11266076;
RA   Gellner K., Eiselt R., Hustert E., Arnold H., Koch I., Haberl M.,
RA   Deglmann C.J., Burk O., Buntefuss D., Escher S., Bishop C.,
RA   Koebe H.-G., Brinkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
RA   Wojnowski L.;
RT   "Genomic organization of the human CYP3A locus: identification of a
RT   new, inducible CYP3A gene.";
RL   Pharmacogenetics 11:111-121(2001).
RN   [7]
RP   SEQUENCE FROM N.A., AND VARIANTS VAL-117 AND ARG-217.
RX   MEDLINE=21098888; PubMed=11181494;
RA   Hsieh K.-P., Lin Y.-Y., Cheng C.-L., Lai M.-L., Lin M.-S.,
RA   Siest J.-P., Huang J.-D.;
RT   "Novel mutations of CYP3A4 in Chinese.";
RL   Drug Metab. Dispos. 29:268-273(2001).
RN   [8]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Zhuge J., Qian Y., Xie H., Yu Y.;
RT   "Sequence of a new human cytochrome P450-3A4 cDNA.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CHARACTERIZATION.
RX   MEDLINE=97243737; PubMed=9088578;
RA   Zhang H., Coville P.F., Walker R.J., Miners J.O., Birkett D.J.,
RA   Wanwimolruk S.;
RT   "Evidence for involvement of human CYP3A in the 3-hydroxylation of
RT   quinine.";
RL   Br. J. Clin. Pharmacol. 43:245-252(1997).
RN   [10]
RP   CHARACTERIZATION.
RX   MEDLINE=98122830; PubMed=9456308;
RA   Zhao X.J., Kawashiro T., Ishizaki T.;
RT   "Mutual inhibition between quinine and etoposide by human liver
RT   microsomes. Evidence for cytochrome P4503A4 involvement in their major
RT   metabolic pathways.";
RL   Drug Metab. Dispos. 26:188-191(1998).
RN   [11]
RP   VARIANTS PRO-221 AND THR-444.
RX   MEDLINE=20132287; PubMed=10668853; DOI=10.1067/mcp.2000.104391;
RA   Sata F., Sapone A., Elizondo G., Stocker P., Miller V.P., Zheng W.,
RA   Raunio H., Crespi C.L., Gonzalez F.J.;
RT   "CYP3A4 allelic variants with amino acid substitutions in exons 7 and
RT   12: evidence for an allelic variant with altered catalytic activity.";
RL   Clin. Pharmacol. Ther. 67:48-56(2000).
RN   [12]
RP   VARIANTS GLN-161; SER-188; PRO-292; THR-444 AND SER-466, AND
RP   CHARACTERIZATION OF THE VARIANTS.
RX   MEDLINE=21571796; PubMed=11714865;
RA   Dai D., Tang J., Rose R., Hodgson E., Bienstock R.J.,
RA   Mohrenweiser H.W., Goldstein J.A.;
RT   "Identification of variants of CYP3A4 and characterization of their
RT   abilities to metabolize testosterone and chlorpyrifos.";
RL   J. Pharmacol. Exp. Ther. 299:825-831(2001).
RN   [13]
RP   VARIANTS ASP-55; GLN-129; ILE-169; HIS-173; MET-362; PHE-372 AND
RP   LEU-415.
RX   MEDLINE=21364010; PubMed=11470997;
RA   Eiselt R., Domanski T.L., Zibat A., Mueller R., Presecan-Siedel E.,
RA   Hustert E., Zanger U.M., Brockmoller J., Klenk H.-P., Meyer U.A.,
RA   Khan K.K., He Y.-A., Halpert J.R., Wojnowski L.;
RT   "Identification and functional characterization of eight CYP3A4
RT   protein variants.";
RL   Pharmacogenetics 11:447-458(2001).

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RN   [14]
RP   VARIANTS PRO-14; GLN-161; HIS-173; SER-184 AND PHE-372.
RX   MEDLINE=21864884; PubMed=11875366;
RA   Lamba J.K., Lin Y.S., Thummel K., Daly A., Watkins P.B., Strom S.,
RA   Zhang J., Schuetz E.G.;
RT   "Common allelic variants of cytochrome P4503A4 and their prevalence in
RT   different populations.";
RL   Pharmacogenetics 12:121-132(2002).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It performs a variety
CC       of oxidation reactions (e.g. caffeine 8-oxidation, omeprazole
CC       sulphoxidation, midazolam 1'-hydroxylation and midazolam 4-
CC       hydroxylation) of structurally unrelated compounds, including
CC       steroids, fatty acids, and xenobiotics. The enzyme also
CC       hydroxylates etoposide.
CC   -!- CATALYTIC ACTIVITY: Quinine + NADPH + O(2) = 3-hydroxyquinine +
CC       NADP(+) + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: Expressed in prostate and liver.
CC   -!- INDUCTION: P450 can be induced to high levels in liver and other
CC       tissues by various foreign compounds, including drugs, pesticides,
CC       and carcinogens.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   -!- DATABASE: NAME=Cytochrome P450 Allele Nomenclature Committee;
CC       NOTE=CYP3A4 alleles;
CC       WWW="http://www.imm.ki.se/CYPalleles/cyp3a4.htm".
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M18907; AAA35745.1; -.
DR   EMBL; M14096; AAA35744.1; -.
DR   EMBL; X12387; CAA30944.1; -.
DR   EMBL; J04449; AAA35747.1; -.
DR   EMBL; AF182273; AAF13598.1; -.
DR   EMBL; AF280107; AAG32290.1; -.
DR   EMBL; AF209389; AAF21034.1; -.
DR   PIR; A29815; A29815.
DR   HSSP; P14779; 1JPZ.
DR   Genew; HGNC:2637; CYP3A4.
DR   MIM; 124010; -.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0019825; F:oxygen binding; TAS.
DR   GO; GO:0006629; P:lipid metabolism; TAS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; NADP; Oxidoreductase; Polymorphism.
FT   INIT_MET      0      0       By similarity.
FT   METAL       441    441       Iron (heme axial ligand) (By similarity).
FT   VARIANT      14     14       L -> P (in allele CYP3A4*14).
FT                                /FTId=VAR_011597.
FT   VARIANT      55     55       G -> D (in allele CYP3A4*7).
FT                                /FTId=VAR_011598.
FT   VARIANT     117    117       I -> V (in allele CYP3A4*4).
FT                                /FTId=VAR_011599.
FT   VARIANT     129    129       R -> Q (in allele CYP3A4*8).
FT                                /FTId=VAR_011600.
FT   VARIANT     161    161       R -> Q (in allele CYP3A4*15).
FT                                /FTId=VAR_011601.
FT   VARIANT     169    169       V -> I (in allele CYP3A4*9).
FT                                /FTId=VAR_011602.
FT   VARIANT     173    173       D -> H (in allele CYP3A4*10).
FT                                /FTId=VAR_011603.
FT   VARIANT     184    184       T -> S (in allele CYP3A4*16).
FT                                /FTId=VAR_011604.
FT   VARIANT     188    188       F -> S (in allele CYP3A4*17; exhibits
FT                                lower turnover numbers for testosterone
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Query Match 98.1%; Score 2494; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 1.2e-173;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 203

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 263

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 323

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 383

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 502
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RESULT 3
CP33_HUMAN
ID   CP33_HUMAN     STANDARD;      PRT;   503 AA.
AC   P05184;
DT   13-AUG-1987 (Rel. 05, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A3 (EC 1.14.14.1) (CYPIIIA3) (HLp).
GN   Name=CYP3A3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=86259780; PubMed=3460094;
RA   Molowa D.T., Schuetz E.G., Wrighton S.A., Watkins P.B., Kremers P.,
RA   Mendez-Picon G., Parker G.A., Guzelian P.S.;
RT   "Complete cDNA sequence of a cytochrome P-450 inducible by
RT   glucocorticoids in human liver.";
RL   Proc. Natl. Acad. Sci. U.S.A. 83:5311-5315(1986).
RN   [2]
RP   SEQUENCE OF 1-20.
RC   TISSUE=Liver;
RX   MEDLINE=85298342; PubMed=3898085;
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RA   Watkins P.B., Wrighton S.A., Maurel P., Schuetz E.G., Mendez-Picon G.,
RA   Parker G.A., Guzelian P.S.;
RT   "Identification of an inducible form of cytochrome P-450 in human
RT   liver.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:6310-6314(1985).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It oxidizes a variety
CC       of structurally unrelated compounds, including steroids, fatty
CC       acids, and xenobiotics.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: By glucocorticoids.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00003; BAA00001.1; -.
DR   EMBL; M13785; AAA35742.1; -.
DR   PIR; A29410; A29410.
DR   HSSP; P14779; 1JPZ.
DR   Genew; HGNC:2636; CYP3A3.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0005792; C:microsome; TAS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0019825; F:oxygen binding; TAS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KW   Heme; Membrane; Microsome; Monooxygenase; Oxidoreductase.
FT   INIT_MET      0      0
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   503 AA;  57428 MW;  9B85D1F729658FC0 CRC64;

  Query Match             96.4%;  Score 2449.5;  DB 1;  Length 503;
  Best Local Similarity   97.9%;  Pred. No. 2.2e-170;
  Matches  470;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         24 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         84 TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||| |||||||||||||||||:|||||:|||||||||| |
Db        144 MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV 203

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        204 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKAVKRMKESRLEDT 263

Qy        243 QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              |||||||||||||| :||||||||||||||||||||||||||||||||||||||||||||
Db        264 QKHRVDFLQLMIDSHKNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 323

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 383

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 NGMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 443

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 4
CP38_MACFA
ID   CP38_MACFA     STANDARD;      PRT;   503 AA.
AC   P33268; P25231;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A8 (EC 1.14.14.1) (CYPIIIA8) (P450-MKNF2) (P-450-
DE   MK2).
GN   Name=CYP3A8;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=93129612; PubMed=1282830; DOI=10.1016/0167-4781(92)90113-E;
RA   Komori M., Kikuchi O., Sakuma T., Funaki J., Kitada M., Kamataki T.;
RT   "Molecular cloning of monkey liver cytochrome P-450 cDNAs: similarity
RT   of the primary sequences to human cytochromes P-450.";
RL   Biochim. Biophys. Acta 1171:141-146(1992).
RN   [2]
RP   SEQUENCE OF 1-22.
RC   TISSUE=Liver;
RX   MEDLINE=89287352; PubMed=2500151; DOI=10.1016/0167-4838(89)90107-6;
RA   Ohta K., Kitada M., Hashizume T., Komori M., Ohi H., Kamataki T.;
RT   "Purification of cytochrome P-450 from polychlorinated biphenyl-
RT   treated crab-eating monkeys: high homology to a form of human
RT   cytochrome P-450.";
RL   Biochim. Biophys. Acta 996:142-145(1989).
CC   -!- FUNCTION: Catalyzes nifedipine and nilvadipine oxidations.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: By polychlorinated biphenyl (PCB).
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S53047; AAB24952.1; -.
DR   PIR; S28168; S28168.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
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KW   Direct protein sequencing; Electron transport; Endoplasmic reticulum;
KW   Heme; Membrane; Microsome; Monooxygenase; Oxidoreductase.
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   503 AA;  57511 MW;  D701B6FE83AC8BFB CRC64;

  Query Match             93.3%;  Score 2372;  DB 1;  Length 503;
  Best Local Similarity   93.9%;  Pred. No. 1e-164;
  Matches  450;  Conservative   18;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||||| ||||||| |||  |||||:||||||||||||:||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGFWTFDMECYKKYGKVWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:|||||||||||||||||||||||:||||||||||:||||||||||||||||||||
Db         85 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||:|||:||||||||| :||||||:||||||||:||||||:||
Db        205 ENTKKLLRFDFLDPFFLSITIFPFIIPILEVLNISIFPREVTSFLRKSVKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||| ||||||||||||||||||||||||||:||||||||||||||||||||
Db        325 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMVVNETLRIFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||| ||||| |||||||||||||| ||||||||||||||||||||||
Db        385 GIFIPKGVVVMIPSYALHHDPKYWPEPEKFLPERFSKKNNDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||:|||||||||||||||||||| |||||| |||:|||:||||||||||
Db        445 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 503


RESULT 5
Q6VP01
ID   Q6VP01      PRELIMINARY;      PRT;   503 AA.
AC   Q6VP01;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cytochrome P450 3A64.
GN   Name=CYP3A64;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Booth-Genthe C.L., Rushmore T.H.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   EMBL; AY334551; AAP94642.1; -.
DR   GO; GO:0004497; F:monooxygenase activity; IEA.
DR   GO; GO:0016712; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   503 AA;  57511 MW;  D701B6FE83AC8BFB CRC64;

  Query Match             93.3%;  Score 2372;  DB 2;  Length 503;
  Best Local Similarity   93.9%;  Pred. No. 1e-164;
  Matches  450;  Conservative   18;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||||| ||||||| |||  |||||:||||||||||||:||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGFWTFDMECYKKYGKVWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:|||||||||||||||||||||||:||||||||||:||||||||||||||||||||
Db         85 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||:|||:||||||||| :||||||:||||||||:||||||:||
Db        205 ENTKKLLRFDFLDPFFLSITIFPFIIPILEVLNISIFPREVTSFLRKSVKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||| ||||||||||||||||||||||||||:||||||||||||||||||||
Db        325 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMVVNETLRIFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||| ||||| |||||||||||||| ||||||||||||||||||||||
Db        385 GIFIPKGVVVMIPSYALHHDPKYWPEPEKFLPERFSKKNNDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||:|||||||||||||||||||| |||||| |||:|||:||||||||||
Db        445 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 503


RESULT 6
Q6PSM4
ID   Q6PSM4      PRELIMINARY;      PRT;   503 AA.
AC   Q6PSM4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cytochrome P450 3A64 variant 1.
GN   Name=CYP3A64;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Booth-Genthe C.L., Rushmore T.H.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   EMBL; AY582531; AAS91645.1; -.
DR   GO; GO:0004497; F:monooxygenase activity; IEA.
DR   GO; GO:0016712; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   503 AA;  57526 MW;  E5206E2DAD8BAE28 CRC64;
```

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  Query Match           93.1%;  Score 2366;  DB 2;  Length 503;
  Best Local Similarity  93.7%;  Pred. No. 2.7e-164;
  Matches  449;  Conservative   18;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||| ||||||| ||| |||||:||||||||||||:||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGFWTFDMECYKKYGKVWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:|||||||||||||||||||||||:||||||||||:|||||||||||||||||||||
Db         85 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||:|||:|||||||||  :||||||:||||||||:|||||:||
Db        205 ENTKKLLRFDFLDPPFLSITIFPPFIIPILEVLNISIFPREVTSFLRKSVKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||||||||||||||||||||| ||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDQELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||| ||||||||||||||||||||||||||:||||||||||||||||||||
Db        325 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMVVNETLRIFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||||| ||||| |||||||||||||| ||||||||||||||||||||
Db        385 GIFIPKGVVVMIPSYALHHDPKYWPEPEKFLPERFSKKNNDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||:|||||||||||||||||||| |||||| |||:|||:||||||||||
Db        445 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 503


RESULT 7
CP3L_CALJA
ID   CP3L_CALJA     STANDARD;      PRT;   503 AA.
AC   O18993;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A21 (EC 1.14.14.1) (CYPIIIA21) (P450 CM3A-10).
GN   Name=CYP3A21;
OS   Callithrix jacchus (Common marmoset).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX   NCBI_TaxID=9483;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=97223367; PubMed=9056237; DOI=10.1006/abbi.1996.9852;
RA   Igarashi T., Sakuma T., Isogai M., Nagata R., Kamataki T.;
RT   "Marmoset liver cytochrome P450s: study for expression and molecular
RT   cloning of their cDNAs.";
RL   Arch. Biochem. Biophys. 339:85-91(1997).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It oxidizes a variety
CC       of structurally unrelated compounds, including steroids, fatty
CC       acids, and xenobiotics.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: P450 can be induced to high levels in liver and other
CC       tissues by various foreign compounds, including drugs, pesticides,
CC       and carcinogens.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D31921; BAA22156.1; -.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; Oxidoreductase.
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   503 AA;  57564 MW;  9BFD421D72C76D6A CRC64;

  Query Match           89.8%;  Score 2283;  DB 1;  Length 503;
  Best Local Similarity  90.0%;  Pred. No. 3.2e-158;
  Matches  431;  Conservative   26;  Mismatches   22;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||||||| :| | :||  |||||:|||||:|| |||:||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGTVLYYRQGFWKFDMECYKKYGKMWGIYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||::|||||||||||||||||||||||||||||||||:|:||||:|||||||||||||
Db         85 TDPNIIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAQDDEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||:|||||||||| |||: :||:|||||||||| ||||||||||||||||||
Db        145 MVPIIAQYGEVLVRNLRREAEKGKPINMKDIFGAYSMDVITGTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |:|||||||||||||||:|||| |||| ||| :|||: |:||||:||:|||||:||
Db        205 ESTKKLLRFDFLDPPFLSITIFPPFLTPILEALNISMFPRDSTSFLRKSIKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||||||||||| ||||||||||||||||||||||||||||| ||||||||||
Db        265 HKHRVDFLQLMIDSQNSKETESDKALSDLELVAQSIIFIFAGYETTSSTLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||| ||||||||||||||||||||||:|||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPATYDTVLQMEYLDMVVNETLRLFPLAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||||| |||||||||||||||| |||||||||||:|||||||
Db        385 GVFIPKGVVVMIPSYALHYDPKYWTEPEKFLPERFSKNNKDNIDPYIYTPFGTGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||| |||||| |||:||||| ||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKVEPRDGTVSGA 503


RESULT 8
CP37_HUMAN
ID   CP37_HUMAN     STANDARD;      PRT;   503 AA.
AC   P24462;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A7 (EC 1.14.14.1) (CYPIIIA7) (P450-HFLA).
GN   Name=CYP3A7;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal liver;
RX   MEDLINE=89255154; PubMed=2722762;
RA   Komori M., Nishio K., Ohi H., Kitada M., Kamataki T.;
RT   "Molecular cloning and sequence analysis of cDNA containing the entire
RT   coding region for human fetal liver cytochrome P-450.";
RL   J. Biochem. 105:161-163(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21163842; PubMed=11266076;
RA   Gellner K., Eiselt R., Hustert E., Arnold H., Koch I., Haberl M.,
RA   Deglmann C.J., Burk O., Buntefuss D., Escher S., Bishop C.,
RA   Koebe H.-G., Brinkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
RA   Wojnowski L.;
RT   "Genomic organization of the human CYP3A locus: identification of a
RT   new, inducible CYP3A gene.";
RL   Pharmacogenetics 11:111-121(2001).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It oxidizes a variety
CC       of structurally unrelated compounds, including steroids, fatty
CC       acids, and xenobiotics.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: P450 can be induced to high levels in liver and other
CC       tissues by various foreign compounds, including drugs, pesticides,
CC       and carcinogens.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   -!- DATABASE: NAME=Cytochrome P450 Allele Nomenclature Committee;
CC       NOTE=CYP3A7 alleles;
CC       WWW="http://www.imm.ki.se/CYPalleles/cyp3a7.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D00408; BAA00310.1; -.
DR   EMBL; AF280107; AAG32289.1; -.
DR   PIR; JX0062; JX0062.
DR   HSSP; P14779; 1JPZ.
DR   Genew; HGNC:2640; CYP3A7.
DR   MIM; 605340; -.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0019825; F:oxygen binding; TAS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; Oxidoreductase.
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   503 AA;  57470 MW;  087CCEED9BAC314C CRC64;

  Query Match           87.8%;  Score 2233;  DB 1;  Length 503;
  Best Local Similarity   88.7%;  Pred. No. 1.4e-154;
  Matches  425;  Conservative   27;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| :|||||||||||||||||||| ||: ||:  |||||:||| |||| || |||:|||
Db         25 YGTRTHGLFKKLGIPGPTPLPFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPMLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||:|||||||||||:|||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||||||||||||| |||||||||||||||:|||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||||: |||| ||| ||||| |||| ||| ||||:| :|| ||||::|| ||::|
Db        205 ENTKKLLRFNPLDPFVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKET 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||||||||::|:|||||||||:|||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKDSETHKALSDLELMAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||:|:||| |||||||||||||:|||||||||||||||:|||||||||||||||||
Db        325 PDVQQKVQKEIDTVLPNKAPPTYDTVLQLEYLDMVVNETLRLFPVAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |||||||||||||| || |||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||:||||||:|||||||||||||||||||  ||||  |||:||| |||| |||||
Db        445 MRFALVNMKLALVRVLQNFSFKPCKETQIPLKLRFGGLLLTEKPIVLKAESRDETVSGA 503


RESULT 9
Q9H241
ID   Q9H241      PRELIMINARY;      PRT;   535 AA.
AC   Q9H241;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cytochrome P450 variant 3A7.
GN   Name=CYP3A7;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20578884; PubMed=11137287; DOI=10.1016/S0378-1119(00)00470-4;
RA   Finta C., Zaphiropoulos P.G.;
RT   "The human cytochrome P450 3A locus. Gene evolution by capture of
RT   downstream exons.";
RL   Gene 260:13-23(2000).
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   EMBL; AF315325; AAG48618.1; -.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   535 AA;  61492 MW;  D42210E526CE1614 CRC64;

  Query Match           87.1%;  Score 2215;  DB 2;  Length 535;
  Best Local Similarity   88.6%;  Pred. No. 3.2e-153;
  Matches  421;  Conservative   27;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         25 YGTRTHGLFKKLGIPGPTPLPFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPMLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
Db        205 ENTKKLLRFNPLDPFVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKET 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
Db        265 QKHRVDFLQLMIDSQNSKDSETHKALSDLELMAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
Db        325 PDVQQKVQKEIDTVLPNKAPPTYDTVLQLEYLDMVVNETLRLFPVAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
Db        385 GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGT 477
Db        445 MRFALVNMKLALVRVLQNFSFKPCKETQIPLKLRFGGLLLTEKPIVLKAESRDET 499
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RESULT 10
Q7Z448
ID Q7Z448 PRELIMINARY; PRT; 430 AA.
AC Q7Z448;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytochrome P450 (Fragment).
GN Name=CYP3A4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=21839017; PubMed=11726664; DOI=10.1074/jbc.M109175200;
RA Finta C., Zaphiropoulos P.G.;
RT "Intergenic mRNA molecules resulting from trans-splicing.";
RL J. Biol. Chem. 277:5882-5890(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Zaphiropoulos P.G.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AJ563376; CAD91645.1; -.
DR HSSP; P14779; 1JPZ.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; p450; 1.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 1 1
SQ SEQUENCE 430 AA; 49137 MW; C232BF7E2571155C CRC64;

Query Match 87.0%; Score 2212; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.9e-153;
Matches 430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         52 FYDGQQPVLAITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLL 111
Db          1 FYDGQQPVLAITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLL 60

Qy        112 SPTFTSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNI 171
Db         61 SPTFTSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNI 120

Qy        172 DSLNNPQDPFVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSV 231
Db        121 DSLNNPQDPFVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSV 180

Qy        232 KRMKESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSV 291
Db        181 KRMKESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSV 240

Qy        292 LSFIMYELATHPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRL 351
Db        241 LSFIMYELATHPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRL 300

Qy        352 ERVCKKDVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYT 411
Db        301 ERVCKKDVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYT 360

Qy        412 PFGSGPRNCIGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKV 471
Db        361 PFGSGPRNCIGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKV 420

Qy        472 ESRDGTVSGA 481
Db        421 ESRDGTVSGA 430
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RESULT 11
CP35_HUMAN
ID CP35_HUMAN STANDARD; PRT; 502 AA.
AC P20815; Q9HB56;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cytochrome P450 3A5 (EC 1.14.14.1) (CYPIIIA5) (P450-PCN3) (HLp2).
GN Name=CYP3A5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89278095; PubMed=2732228;
RA Aoyama T., Yamano S., Waxman D.J., Lapenson D.P., Meyer U.A.,
RA Fischer V., Tyndale R., Inaba T., Kalow W., Gelboin H.V.,
RA Gonzalez F.J.;
RT "Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIIA gene product
RT that is differentially expressed in adult human liver. cDNA and
RT deduced amino acid sequence and distinct specificities of cDNA-
RT expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and
RT cyclosporine.";
RL J. Biol. Chem. 264:10388-10395(1989).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Liver;
RX PubMed=2802615;
RA Schuetz J.D., Molowa D.T., Guzelian P.S.;
RT "Characterization of a cDNA encoding a new member of the
RT glucocorticoid-responsive cytochromes P450 in human liver.";
RL Arch. Biochem. Biophys. 274:355-365(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 1-106 FROM N.A.
RX   MEDLINE=21163842; PubMed=11266076;
RA   Gellner K., Eiselt R., Hustert E., Arnold H., Koch I., Haberl M.,
RA   Deglmann C.J., Burk O., Buntefuss D., Escher S., Bishop C.,
RA   Koebe H.-G., Brinkmann U., Klenk H.-P., Kleine K., Meyer U.A.,
RA   Wojnowski L.;
RT   "Genomic organization of the human CYP3A locus: identification of a
RT   new, inducible CYP3A gene.";
RL   Pharmacogenetics 11:111-121(2001).
RN   [5]
RP   SEQUENCE OF 1-24 FROM N.A.
RX   MEDLINE=96152836; PubMed=8569713;
RA   Schuetz J.D., Schuetz E.G., Thottassery J.V., Guzelian P.S., Strom S.,
RA   Sun D.;
RT   "Identification of a novel dexamethasone responsive enhancer in the
RT   human CYP3A5 gene and its activation in human and rat liver cells.";
RL   Mol. Pharmacol. 49:63-72(1996).
RN   [6]
RP   VARIANT CYP3A5*2.
RX   MEDLINE=96192071; PubMed=8619878; DOI=10.1006/bbrc.1996.0618;
RA   Jounaidi Y., Hyrailles V., Gervot L., Maurel P.;
RT   "Detection of CYP3A5 allelic variant: a candidate for the polymorphic
RT   expression of the protein?";
RL   Biochem. Biophys. Res. Commun. 221:466-470(1996).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It oxidizes a variety
CC       of structurally unrelated compounds, including steroids, fatty
CC       acids, and xenobiotics.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: P450 can be induced to high levels in liver and other
CC       tissues by various foreign compounds, including drugs, pesticides,
CC       and carcinogens.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   -!- DATABASE: NAME=Cytochrome P450 Allele Nomenclature Committee;
CC       NOTE=CYP3A5 alleles;
CC       WWW="http://www.imm.ki.se/CYPalleles/cyp3a5.htm".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J04813; AAA02993.1; -.
DR   EMBL; BC033862; AAH33862.1; -.
DR   EMBL; AF280107; AAG32288.1; -.
DR   EMBL; L35912; AAB00083.1; -.
DR   PIR; A34101; A34101.
DR   HSSP; P14779; 1JPZ.
DR   Genew; HGNC:2638; CYP3A5.
DR   H-InvDB; HIX0006899; -.
DR   MIM; 605325; -.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0005792; C:microsome; TAS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0019825; F:oxygen binding; TAS.
DR   GO; GO:0008202; P:steroid metabolism; TAS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; Oxidoreductase; Polymorphism.
FT   METAL       441    441       Iron (heme axial ligand).
FT   VARIANT     398    398       T -> N (in allele CYP3A5*2).
FT                                /FTId=VAR_008365.
FT   CONFLICT    305    305       A -> P (in Ref. 2).
FT   CONFLICT    318    318       L -> F (in Ref. 2).
FT   CONFLICT    324    324       H -> D (in Ref. 2).
FT   CONFLICT    377    377       C -> G (in Ref. 2).
SQ   SEQUENCE   502 AA;  57108 MW;  D5A2302E2633E717 CRC64;

  Query Match             84.3%;  Score 2142.5;  DB 1;  Length 502;
  Best Local Similarity   84.1%;  Pred. No. 5.8e-148;
  Matches  402;  Conservative   37;  Mismatches   38;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| :|||||:|||||||||| |||:||| :|   || ||:||||||:|| |:|| |||||
Db         25 YGTRTHGLFKRLGIPGPTPLPLLGNVLSYRQGLWKFDTECYKKYGKMWGTYEGQLPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||:|:|||||||||||||||  ||||||||||:||||||||:|||||||||||||||
Db         85 TDPDVIRTVLVKECYSVFTNRRSLGPVGFMKSAISLAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | |||||||||||||||||| ||||||||:|||||||||| ||||||||||||||||||
Db        145 MFPIIAQYGDVLVRNLRREAEKGKPVTLKDIFGAYSMDVITGTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |:||| |:| |||| |||| :|||| |: | ||: :||::  ||| ||| |||:||| |
Db        205 ESTKKFLKFGFLDPLFLSIILFPFLTPVFEALNVSLFPKDTINFLSKSVNRMKKSRLNDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||:|||||||||||||||||||||||||| |||||||||||||||||| :||||||
Db        265 QKHRLDFLQLMIDSQNSKETESHKALSDLELAAQSIIFIFAGYETTSSVLSFTLYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||:|||||||||||||||:|:|||||||||||||||:|:|||| ||||||||
Db        325 PDVQQKLQKEIDAVLPNKAPPTYDAVVQMEYLDMVVNETLRLFPVAIRLERTCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| :|:||:|||| |||||||||:| ||||||| ||:|||||||||:|||||||
Db        385 GVFIPKGSMVVIPTYALHHDPKYWTEPEEFRPERFSKK-KDSIDPYIYTPFGTGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||||||||||||||||||||||||||||    ||||||||:||||:|||||:||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLDTQGLLQPEKPIVLKVDSRDGTLSG 501


RESULT 12
Q6GUQ3
ID   Q6GUQ3      PRELIMINARY;      PRT;   503 AA.
AC   Q6GUQ3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Cytochrome P450 CYP3A66.
GN   Name=CYP3A66;
```

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OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Carr B.A., Fang Y., Rushmore T.H.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   EMBL; AY635466; AAT49270.1; -.
DR   GO; GO:0004497; F:monooxygenase activity; IEA.
DR   GO; GO:0016712; F:oxidoreductase activity, acting on paired d. . .; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   503 AA;  57382 MW;  D0B8902ADDF33810 CRC64;

  Query Match             83.1%;  Score 2112;  DB 2;  Length 503;
  Best Local Similarity   83.5%;  Pred. No. 9.8e-146;
  Matches  399;  Conservative   34;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| |:|||||: |||||||||||||||| :|   || ||:|||||:|   ||| ||| |
Db         25 YGTRSYGLFKRQGIPGPTPLPFLGNILSYRQGLWKFDTECYKKYGKMWRTQDGQLPVLTI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:||||||||||||||||| |||| |||||||||||||:|||||||||||||||||
Db         85 TDPEMIKTVLVKECYSVFTNRRPLGPVGLMKSAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | |||||||:|||||||||| |||||||:||||||||||||||||||||||:||||
Db        145 MFPIIAQYGDMLVRNLRREAEKGKPVTLKDIFGAYSMDVITSTSFGVNIDSLNNPKDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |: || |:|||||| ||   :|||| |  | ||: :||::  ||| |||  ||:||| |
Db        205 ESVKKFLKFDFLDPLFLLTILFPFLTPAFEALNVSLFPKDAINFLNKSVNSMKKSRLNDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||| ||||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDQELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||:|||||||||| ||| ::|||||||||||||||||:|||| ||||||||
Db        325 PDVQQKLQKEIDAVLPNKAPATYDAMVQMEYLDMVVNETLRLFPIAIRLERACKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||| :|:||:|||| |||||||||:| ||||||||||:||||||||||:|||||||
Db        385 GVFIPKGAMVVIPTYALHHDPKYWTEPEEFRPERFSKKNKDSIDPYIYTPFGTGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||||||||:|:|||||||||||||||   |||| |||:||||||||||:||
Db        445 MRFALMNMKLAIIKVLQNFSFKPCKETQIPLKLGNQGLLQSEKPIVLKVESRDGTLSG 502


RESULT 13
CP3C_CANFA
ID   CP3C_CANFA     STANDARD;      PRT;   503 AA.
AC   P24463;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A12 (EC 1.14.14.1) (CYPIIIA12) (P450-PBD-1).
GN   Name=CYP3A12;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Beagle; TISSUE=Liver;
RX   MEDLINE=91159488; PubMed=2001406; DOI=10.1016/0167-4781(91)90072-T;
RA   Ciaccio P.J., Graves P.E., Bourque D.P., Glinsmann-Gibson B.,
RA   Halpert J.R.;
RT   "cDNA and deduced amino acid sequences of a dog liver cytochrome P-450
RT   of the IIIA gene subfamily.";
RL   Biochim. Biophys. Acta 1088:319-322(1991).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. In liver microsomes, this enzyme is involved in an
CC       NADPH-dependent electron transport pathway. It oxidizes a variety
CC       of structurally unrelated compounds, including steroids, fatty
CC       acids, and xenobiotics.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- INDUCTION: P450 can be induced to high levels in liver and other
CC       tissues by various foreign compounds, including drugs, pesticides,
CC       and carcinogens.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X54915; CAA38687.1; -.
DR   PIR; S14275; S14275.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; Oxidoreductase.
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   503 AA;  57721 MW;  52171D03F9BD5D87 CRC64;

  Query Match             81.7%;  Score 2077;  DB 1;  Length 503;
  Best Local Similarity   79.7%;  Pred. No. 3.5e-143;
  Matches  382;  Conservative   55;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||::||:|:|||||||||||:|  | |  || :|||:|  |||::|||||:||||||
Db         25 YGTYTHGIFRKLGIPGPTPLPFVGTALGYRNGFYVFDMKCFSKYGRMWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||  ||||||||||::|||||||:|:|||||||:|||||
Db         85 TDPDMIKTVLVKECYSVFTNRRTLGPVGFMKSAISLSEDEEWKRMRTLLSPTFTTGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||| ||||||| |||:||| || : |||||||||||||||||||||||:||||||
Db        145 MFPIIGQYGDVLVNNLRKEAEKGKAINLKDVFGAYSMDVITSTSFGVNIDSLNHPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||:|||||||| || :|||| |: |:||| :||::||:| ||||:|||||||:|
Db        205 ENTKKLLKFDFLDPFFFSILLFPFLTPVFEILNIWLFPKKVTDFFRKSVERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||:|||||| ::|||||||||||||||||||||||: |||:|||||||
```

```
Db        265 QKHRVDFLQLMINSQNSKEMDTHKALSDLELVAQSIIFIFAGYETTSTSLSFLMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||  |||| |||| ::||||||||:||||||:||| ||||||||||||:
Db        325 PDVQQKLQEEIDATFPNKALPTYDALVQMEYLDMVLNETLRLYPIAGRLERVCKKDVEIS 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| |||:|:: ||||    | |||:| |||||:||||:|:|| | |||:|||||||
Db        385 GVFIPKGTVVMVPTFTLHRDQSLWPEPEEFRPERFSRKNKDSINPYTYLPFGTGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||:|||||||:||||||||||||||||||:  |::|||||:||||| |||:|:||
Db        445 MRFAIMNMKLALVRVLQNFSFKPCKETQIPLKLNAQGIIQPEKPIVLKVEPRDGSVNGA 503


RESULT 14
Q8HZK1
ID   Q8HZK1      PRELIMINARY;      PRT;   503 AA.
AC   Q8HZK1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cytochrome P450 3A26.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=98064129; PubMed=9400018;
RA   Fraser D.J., Feyereisen R., Harlow G.R., Halpert J.R.;
RT   "Isolation, heterologous expression and functional characterization of
RT   a novel cytochrome P450 3A enzyme from a canine liver cDNA library.";
RL   J. Pharmacol. Exp. Ther. 283:1425-1432(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Fraser D.J., Feyereisen R., Harlow G.R., Halpert J.R.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR   EMBL; AF547269; AAN47145.1; -.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW   Heme; Monooxygenase; Oxidoreductase.
SQ   SEQUENCE   503 AA;  57726 MW;  AFBC66002CC7CA67 CRC64;

  Query Match             79.7%;  Score 2025;  DB 2;  Length 503;
  Best Local Similarity   77.9%;  Pred. No. 2.2e-139;
  Matches  373;  Conservative   57;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||::||:|:|||||||||||||:|  | |  || :|||:|  |||::|||||:||||||
Db         25 YGTYTHGIFRKLGIPGPTPLPFVGTALGYRNGFYVFDMKCFSKYGRMWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||||||  ||||||||||::|||||:|:|||||||:||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRTLGPVGFMKSAISLSEDEEWKRIRTLLSPTFTTGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||| ||||||| |||:||| || : |||||||||||||| ||||||||||:||||||
Db        145 MFPIIGQYGDVLVNNLRKEAEKGKAINLKDVFGAYSMDVITSISFGVNIDSLNHPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||| ||:|||||||  || :|||| |: |:||| :||::||:| ||||:|||||||:|
Db        205 ENTKNLLKFDFLDPFLFSILLFPFLTPVFEILNIWLFPKKVTDFFRKSVERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||:|||||| ::|||||||||||||:|||||||||| |||:|||||||
Db        265 QKHRVDFLQLMINSQNSKEMDTHKALSDLELVAQSIVFIFAGYETTSSCLSFLMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||  |||| |||: ::|||||||:||||||: :| ||||||||||||:
Db        325 RDVQQKLQEEIDATFPNKAAPTYEALVQMEYLDMVLNETLRLYSVAGRLERVCKKDVEIS 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| |||:|:: ||||    | |||:| |||||:||||:|:|| | |||:|||||||
Db        385 GVFIPKGTVVMVPTFILHRDQNLWPEPEEFRPERFSRKNKDSINPYTYLPFGTGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||:|||||||:|||||||| |||||| |::  |::||||||||||| |||:||||
Db        445 MRFAIMNMKLALVRVLQNFSFKSCKETQISLRINTRGIIQPEKPVVLKVEPRDGSVSGA 503


RESULT 15
CP39_RAT
ID   CP39_RAT       STANDARD;      PRT;   503 AA.
AC   P51538; Q64557; Q64631;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Cytochrome P450 3A9 (EC 1.14.14.1) (CYPIIIA9) (P450-OLF3) (Olfactive)
DE   (3AH15).
GN   Name=Cyp3a9;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=97144501; PubMed=8990268; DOI=10.1006/abbi.1996.9752;
RA   Mahnke A., Strotkamp D., Roos P.H., Hanstein W.G., Chabot G.G.,
RA   Nef P.;
RT   "Expression and inducibility of cytochrome P450 3A9 (CYP3A9) and other
RT   members of the CYP3A subfamily in rat liver.";
RL   Arch. Biochem. Biophys. 337:62-68(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96220175; PubMed=8660328; DOI=10.1006/bbrc.1996.0562;
RA   Wang H., Kawashima H., Strobel H.W.;
RT   "cDNA cloning of a novel CYP3A from rat brain.";
RL   Biochem. Biophys. Res. Commun. 221:157-162(1996).
CC   -!- FUNCTION: This isozyme seems to be implicated in olfaction. Active
CC       in the demethylation of erythromycin as well as benzphetamine.
CC   -!- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
CC       oxidized flavoprotein + H(2)O.
CC   -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC   -!- TISSUE SPECIFICITY: Mainly expressed in olfactory epithelium.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U60085; AAB03662.1; -.
DR   EMBL; U46118; AAC52582.1; -.
DR   PIR; JC4702; JC4702.
DR   HSSP; P14779; 1JPZ.
DR   GO; GO:0005624; C:membrane fraction; ISS.
DR   GO; GO:0004497; F:monooxygenase activity; ISS.
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DR   GO; GO:0006805; P:xenobiotic metabolism; ISS.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR008072; EP450_CYP3A.
DR   InterPro; IPR002401; EP450I.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR01689; EP450IICYP3A.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Electron transport; Endoplasmic reticulum; Heme; Membrane; Microsome;
KW   Monooxygenase; Olfaction; Oxidoreductase.
FT   METAL       442    442       Iron (heme axial ligand) (By similarity).
FT   CONFLICT    457    457       F -> V (in Ref. 2).
SQ   SEQUENCE   503 AA;  57811 MW;  9BBB13E690675EB4 CRC64;

  Query Match             78.7%;  Score 2000;  DB 1;  Length 503;
  Best Local Similarity   76.6%;  Pred. No. 1.5e-137;
  Matches  367;  Conservative   60;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||:|||||||||| |||||| ||:| |||  ||  |||||||:|| |||:||||||
Db         25 YGTHSHGIFKKLGIPGPKPLPFLGTILAYRKGFWEFDKYCHKKYGKLWGLYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||:|||||||||||| ||||| ||||| :| ||||:|||||||:|:|||||||||||||
Db         85 TDPDIIKTVLVKECYSTFTNRRNFGPVGILKKAISISEDEEWKRIRALLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||| || |:||||:|: :| ||| ::||:||||||||||:|||||:|||||||||||
Db        145 MFPIINQYTDMLVRNMRQGSEEGKPTSMKDIFGAYSMDVITATSFGVNVDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |  ||||:||  || |||:|:|||| |: | ||: :|||:| :| : ||:||||:|:::
Db        205 EKVKKLLKFDIFDPLFLSVTLFPFLTPLFEALNVSMFPRDVIDFFKTSVERMKENRMKEK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              :| |:|||||||:|||||  :|||||||:|:||||:||||||||||| |||::| || |
Db        265 EKQRMDFLQLMINSQNSKVKDSHKALSDVEIVAQSVIFIFAGYETTSSALSFVLYLLAIH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||:|:|||:|||| |||||  ||||:|||||||||||||||:||| ||||||| |||||
Db        325 PDIQKKLQDEIDAALPNKAHATYDTLLQMEYLDMVVNETLRLYPIAGRLERVCKTDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| |||||::|||:|| || |||:| ||||||||:|||:||:| |||:|||||||
Db        385 GVFIPKGTVVMIPTFALHKDPHYWPEPEEFRPERFSKKNQDNINPYMYLPFGNGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||:|| |||||||:|||||||||||  ||||||||::||| ||| ||:||
Db        445 MRFALMNMKVALFRVLQNFSFQPCKETQIPLKLSKQGLLQPEKPLLLKVVSRDETVNGA 503


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Job time : 178 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:23 ; Search time 167 Seconds
(without alignments)
1123.226 Million cell updates/sec

Title: US-10-690-991-2
Perfect score: 2542
Sequence: 1 MAYGTHSHGLFKKLGIPGPT.....PVVLKVESRDGTVSGAHHHH 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2542	100.0	485	8	ADO33768	Ado33768 Human CYP
2	2533	99.6	485	8	ADJ87521	Adj87521 Human cyt
3	2501	98.4	503	5	ABG68753	Abg68753 Cytochrom
4	2501	98.4	503	6	ABU57260	Abu57260 Human chy
5	2501	98.4	503	6	ABR82024	Abr82024 Human cyt
6	2501	98.4	503	8	ADL18578	Adl18578 Human wil
7	2501	98.4	503	8	ADL18672	Adl18672 Human cyt
8	2494	98.1	502	7	ADD48378	Add48378 Human Pro
9	2494	98.1	503	2	AAR72363	Aar72363 Human cyt
10	2494	98.1	503	2	AAR81464	Aar81464 Human der
11	2494	98.1	503	2	AAR93170	Aar93170 Human cyt
12	2494	98.1	503	2	AAY05202	Aay05202 Human CYP
13	2494	98.1	503	8	ADQ89978	Adq89978 Antagonis
14	2466	97.0	502	8	ADO47239	Ado47239 Human cyt
15	2449.5	96.4	503	8	ADO47238	Ado47238 Human cyt
16	2386	93.9	498	8	ABM83111	Abm83111 Human dia
17	2327.5	91.6	489	8	ABM83114	Abm83114 Human dia
18	2282	89.8	480	8	ABM83112	Abm83112 Human dia
19	2259	88.9	478	8	ABM83113	Abm83113 Human dia
20	2233	87.8	503	5	AAE22852	Aae22852 Human cyt
21	2233	87.8	503	8	ADO47243	Ado47243 Human cyt
22	2215	87.1	535	5	ABG68747	Abg68747 Cytochrom
23	2212	87.0	454	5	ABG68754	Abg68754 Cytochrom
24	2178	85.7	464	8	ABM83115	Abm83115 Human dia
25	2142.5	84.3	502	5	AAE26192	Aae26192 Human cyt
26	2142.5	84.3	502	7	ADE57186	Ade57186 Human Pro
27	2142.5	84.3	502	7	ADE57190	Ade57190 Human Pro
28	2142.5	84.3	502	7	ADE63919	Ade63919 Human Pro
29	2142.5	84.3	502	8	ADJ75595	Adj75595 Marker ge
30	2142.5	84.3	502	8	ADN04176	Adn04176 Antipsori
31	2142.5	84.3	502	8	ADO47240	Ado47240 Human cyt
32	2077	81.7	503	8	ADO47244	Ado47244 Dog cytoc
33	2007	79.0	465	8	ADL90232	Adl90232 Human enz
34	1989	78.2	501	8	ADO47242	Ado47242 Rabbit cy
35	1983	78.0	503	8	ADO47245	Ado47245 Pig cytoc
36	1970	77.5	562	4	AAU30319	Aau30319 Novel hum
37	1961	77.1	503	8	ADO47246	Ado47246 Murine cy
38	1958	77.0	502	5	ABB07519	Abb07519 Human dru
39	1957	77.0	503	6	ABU07859	Abu07859 Human cyt
40	1957	77.0	503	8	ADG20513	Adg20513 Human cyt
41	1957	77.0	503	8	ADO47241	Ado47241 Human cyt
42	1956	76.9	503	8	ADM87339	Adm87339 Human pro
43	1946.5	76.6	504	6	ABU07860	Abu07860 Human cyt
44	1946.5	76.6	504	7	ADE57188	Ade57188 Rat Prote
45	1946.5	76.6	504	7	ADE63917	Ade63917 Rat Prote

ALIGNMENTS

RESULT 1
ADO33768
ID ADO33768 standard; protein; 485 AA.
XX
AC ADO33768;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human CYP3A4 truncated protein with synthetic N-terminal and His tag.
XX
KW cytochrome P450; CYP3A4; protein co-ordinate data; cytostatic; cancer;
KW hydrophobic transmembrane domain truncated; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1. .16
FT /note= "Synthetic N-terminal region"
FT Region 482. .485
FT /note= "Synthetic His tag"
XX
PN WO2004038015-A1.
XX
PD 06-MAY-2004.
XX
PF 24-OCT-2003; 2003WO-GB004598.
XX
PR 25-OCT-2002; 2002US-0421063P.
PR 19-JUN-2003; 2003US-0479448P.
XX
PA (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI Tickle IJ, Vonrhein C, Williams PA, Jhoti H, Kirton SB;
XX
DR WPI; 2004-440452/41.
DR N-PSDB; ADO33767.
XX
PT Obtaining a representation of the 3-D structure of cytochrome P450 3A4
PT crystals, by providing data of structure factors used to generate
PT electron density map of crystal structure and constructing electron
PT density map of obtained data.
XX
PS Claim 64; SEQ ID NO 2; 357pp; English.
XX
CC The invention relates to a novel method for obtaining a representation of
CC the 3-dimensional structure of a crystal of cytochrome P450 (CYP)3A4
CC which involves providing the data of structural factors and phases used

```
CC   to generate an electron density map of 3A4 crystal structures as given in
CC   specification and constructing an electron density map of the structural
CC   factors and phases. The method of the invention has cytostatic
CC   applications and may be useful for obtaining a representation of the 3-
CC   dimensional structure of a crystal of CYP3A4, where the crystal structure
CC   is useful in modelling the interaction of a compound with the protein and
CC   in drug design. Such information may be utilised on order to generate a
CC   composition to treat cancer. The current sequence is that of the human
CC   CYP3A4 N-terminal truncated protein of the invention which has a
CC   synthetic N-terminal region in place of the hydrophobic transmembrane
CC   domain in order to aid Escherichia coli expression and solubility, in
CC   addition to a C-terminal His tag which facilitates purification.
XX
SQ   Sequence 485 AA;

  Query Match            100.0%;  Score 2542;  DB 8;  Length 485;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-230;
  Matches  485;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60

Qy         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120

Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180

Qy        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240

Qy        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300

Qy        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360

Qy        361 INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC 420

Qy        421 IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480

Qy        481 AHHHH 485
              |||||
Db        481 AHHHH 485


RESULT 2
ADJ87521
ID   ADJ87521 standard; protein; 485 AA.
XX
AC   ADJ87521;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human cytochrome P450 3A4 protein.
XX
KW   cytochrome P450; crystallography.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003102192-A1.
XX
PD   11-DEC-2003.
XX
PF   30-MAY-2002; 2002WO-GB002668.
XX
PR   30-MAY-2002; 2002WO-GB002668.
XX
PA   (ASTE-) ASTEX TECHNOLOGY LTD.
XX
PI   Cosme J,  Ward A,  Vuillard L,  Williams P,  Hamilton B;
XX
DR   WPI; 2004-043119/04.
DR   N-PSDB; ADJ87520.
XX
PT   Purifying a cytochrome P450, for NMR studies and high-throughput
PT   screening methods to discover drugs, comprises suspending cells
PT   expressing P450 molecule in a salt buffer, lysing the cells and providing
PT   a high-salt-detergent lysate.
XX
PS   Claim 12; SEQ ID NO 8; 77pp; English.
XX
CC   The invention relates to a method of purifying a cytochrome P450 by
CC   expressing in a host cell culture a cytochrome P450 molecule, recovering
CC   the cells from the culture and suspending the cells in a salt buffer
CC   having a conductivity of 12-110 mS/cm, lysing the cells and removing cell
CC   debris to provide a high-salt lysate, adding to the lysate a detergent to
CC   provide a high-salt-detergent lysate, and recovering the P450 from the
CC   lysate. Methods of preparing and purifying cytochrome P450 proteins are
CC   useful for X-ray crystallographic studies and crystallographic screening
CC   of small molecules bound to P450, or for NMR studies and high-throughput
CC   screening methods to discover drugs or analyze the interaction of drugs
CC   with P450 molecules. This sequence corresponds to the human cytochrome
CC   P450 3A4.
XX
SQ   Sequence 485 AA;

  Query Match            99.6%;  Score 2533;  DB 8;  Length 485;
  Best Local Similarity   99.8%;  Pred. No. 5e-229;
  Matches  484;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60

Qy         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120

Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180

Qy        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        181 FVENTKKLLRFDFLDPFFLSITVFPELIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240

Qy        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300

Qy        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360

Qy        361 INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC 420

Qy        421 IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480

Qy        481 AHHHH 485
              |||||
```

```
Db        481 AHHHH 485


RESULT 3
ABG68753
ID   ABG68753 standard; protein; 503 AA.
XX
AC   ABG68753;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Cytochrome P450 CYP3A43 exon 1-CYP3A4 exon 2-13.
XX
KW   Cytochrome P450; CYP3AP1; CYP3AP2; CYP3A43; CYP3A4; CYP3A5; CYP3A7;
KW   drug metabolism; drug design; drug screening.
XX
OS   Homo sapiens.
XX
PN   WO200244213-A1.
XX
PD   06-JUN-2002.
XX
PF   28-NOV-2001; 2001WO-SE002631.
XX
PR   28-NOV-2000; 2000SE-00004366.
PR   11-JUN-2001; 2001SE-00002061.
XX
PA   (ZAPH/) ZAPHIROPOULOS P G.
PA   (FINT/) FINTA C.
XX
PI   Zaphiropoulos PG,  Finta C;
XX
DR   WPI; 2002-557532/59.
DR   N-PSDB; ABK97692.
XX
PT   Novel cytochrome P450 protein in which CYP3A43 exon 1 is joined to sets
PT   of CYP3A4 or CYP3A5 exons, useful as medicament, and in evaluating drug
PT   metabolism, in drug design and drug screening.
XX
PS   Claim 2; Fig 11; 131pp; English.
XX
CC   The invention describes a cytochrome P450 protein (I) in which CYP3A43
CC   exon 1 is joined to sets of CYP3A4 or CYP3A5 exons, as well as sub
CC   fragments, variants and multiples of (I) having essentially the same
CC   characteristics. (I) Is useful as a medicament, and for evaluating drug
CC   metabolism, in drug design, and drug screening, and in tests for
CC   adjusting the dose of drugs. This is the amino acid sequence of a novel
CC   cytochrome P450 protein
XX
SQ   Sequence 503 AA;

  Query Match             98.4%;  Score 2501;  DB 5;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-226;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 4
ABU57260
ID   ABU57260 standard; protein; 503 AA.
XX
AC   ABU57260;
XX
DT   25-APR-2003  (first entry)
XX
DE   Human chytochrome P450 CYP3A4 protein.
XX
KW   Human; enzyme; transgenic; drug metabolism; behaviour; mouse;
KW   pharmacokinetic assay; pharmacodynamic assay; toxicology; serum albumin;
KW   alpha-acidic glycoprotein; CYP; multidrug resistance protein; MRP;
KW   uridine diphosphoglucuronosyl transferase; UGT; cytochrome P450.
XX
OS   Homo sapiens.
XX
PN   WO200283897-A1.
XX
PD   24-OCT-2002.
XX
PF   18-APR-2002; 2002WO-AU000485.
XX
PR   18-APR-2001; 2001AU-00004467.
XX
PA   (GENE-) GENE STREAM PTY LTD.
XX
PI   Daly JM;
XX
DR   WPI; 2003-093021/08.
DR   N-PSDB; ABX77172.
XX
PT   New transgenic non-human animal expressing a foreign polypeptide
PT   associated with drug behavior and/or metabolism, useful for studying the
PT   behavior and/or metabolism of a drug in other animals.
XX
PS   Disclosure; Page 299-301; 408pp; English.
XX
CC   This invention relates to a transgenic non-human animal which may be used
CC   for assessing the behaviour and/or metabolism of a drug in another animal
CC   and which expresses a foreign polypeptide associated with drug behaviour
CC   and/or metabolism. The invention also comprises a nucleic acid construct
CC   for use in producing the above transgenic non-human animal and a method
CC   of assessing the metabolism and/or behavior of a drug in an animal of
CC   interest, comprising administering a test agent to the transgenic animal
CC   and conducting analytical tests to determine drug metabolism and/or
CC   behaviour. The transgenic animal is useful in studying drug metabolism
CC   and/or behaviour in other animals. The nucleic acid construct is useful
CC   in producing the above transgenic animal and the methods are used for
CC   producing, breeding and using transgenic animals for pharmacological
CC   (e.g. pharmacokinetic or pharmacodynamic assays) and/or toxicological
CC   studies. Nucleic acid sequences used within the invention are serum
CC   albumin; alpha-acidic glycoprotein; cytochrome P450 (CYP); uridine
CC   diphosphoglucuronosyl transferase (UGT); multidrug resistance proteins
CC   and (MRP's). The present sequence represents a protein sequence used to
CC   create a transgenic animal within the scope of the invention
XX
SQ   Sequence 503 AA;
```

```
  Query Match             98.4%;  Score 2501;  DB 6;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-226;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503
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```
RESULT 5
ABR82024
ID   ABR82024 standard; protein; 503 AA.
XX
AC   ABR82024;
XX
DT   22-SEP-2003  (first entry)
XX
DE   Human cytochrome P450 3A4 amino acid sequence.
XX
KW   Human; protein array; protein moiety; phenotype; drug discovery;
KW   naturally occurring variant; pharmacogenomic; diagnostic;
KW   parallel analysis; tumour suppressor; p53; cytochrome P450.
XX
OS   Homo sapiens.
XX
PN   WO2003048768-A2.
XX
PD   12-JUN-2003.
XX
PF   05-DEC-2002; 2002WO-GB005499.
XX
PR   05-DEC-2001; 2001US-0335806P.
PR   16-SEP-2002; 2002US-0410815P.
XX
PA   (SENS-) SENSE PROTEOMIC LTD.
XX
PI   Boutell JM,  Godber BLJ,  Hart DJ,  Blackburn JD;
XX
DR   WPI; 2003-569063/53.
DR   N-PSDB; ACF06054.
XX
PT   New protein array, useful for determining the phenotype of a naturally
PT   occurring variant of a DNA sequence of interest, comprises a surface upon
PT   which at least two protein moieties are deposited.
XX
PS   Example 5; Fig 11B; 84pp; English.
XX
CC   The present invention describes a protein array comprising a surface upon
CC   which at least two protein moieties are deposited at spatially defined
CC   locations, where the protein moieties are naturally occurring variants of
CC   a DNA sequence of interest. Also described: (1) making a protein array;
CC   (2) screening a set of protein moieties for molecules that interact with
CC   one or more proteins; and (3) simultaneously determining the relative
CC   properties of members of a set of protein moieties. The protein array can
CC   be used for determining the phenotype of a naturally occurring variant of
CC   a DNA sequence of interest. The protein array is useful for drug
CC   discovery, pharmacogenomics and diagnostics. The protein array allows the
CC   parallel analysis of closely related proteins with a sensitivity that is
CC   at least comparable to existing methods, if not better, with small
CC   volumes of potentially expensive ligands, and in a quantitative,
CC   comparative functional analysis manner not previously possible. ACF06000
CC   to ACF06056 and ABR81975 to ABR82026 represent sequences used in the
CC   exemplification of the present invention
XX
SQ   Sequence 503 AA;
```

```
  Query Match             98.4%;  Score 2501;  DB 6;  Length 503;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-226;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503
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RESULT 6
ADL18578
ID   ADL18578 standard; protein; 503 AA.
XX
AC   ADL18578;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human wild-type cytochrome P450 CYP3A4 protein.
XX
KW   drug metabolic activity; CYP3A4; human; wild-type; cytochrome P450; SNP;
KW   single nucleotide polymorphism.
XX
OS   Homo sapiens.
```

```
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 185
FT                   /note= "Thr may be substituted for Ser due to single
FT                   nucleotide polymorphism (SNP) in coding DNA"
FT   Misc-difference 293
FT                   /note= "Leu may be substituted for Pro due to single
FT                   nucleotide polymorphism (SNP) in coding DNA"
FT   Misc-difference 363
FT                   /note= "Thr may be substituted for Met due to single
FT                   nucleotide polymorphism (SNP) in coding DNA"
XX
PN   JP2004000004-A.
XX
PD   08-JAN-2004.
XX
PF   23-APR-2002; 2002JP-00120246.
XX
PR   23-APR-2002; 2002JP-00120246.
XX
PA   (KOKU-) KOKURITSU IYAKUHIN SHOKUHIN EISEI KENKYU.
PA   (IYAK-) IYAKUHIN FUKUSAYO HIGAI KYUSAI KENKYU SH.
XX
DR   WPI; 2004-085203/09.
DR   N-PSDB; ADL18577.
XX
PT   Testing the drug metabolic activity of CYP3A4 such as testosterone
PT   hydroxylase activity by detecting the CYP3A4 gene polymorphisms in which
PT   the drug metabolic activity of CYP3A4 is reduced.
XX
PS   Disclosure; SEQ ID NO 2; 48pp; Japanese.
XX
CC   The invention relates to a novel method for testing the drug metabolic
CC   activity of CYP3A4 by detecting the CYP3A4 gene polymorphisms in which
CC   the drug metabolic activity of CYP3A4 is reduced. The method of the
CC   invention may be useful for testing the possibility of a side effect
CC   resulting from a drug metabolised by CYP3A4 in a subject. The current
CC   sequence is that of the human wild-type cytochrome P450 CYP3A4 protein of
CC   the invention.
XX
SQ   Sequence 503 AA;

  Query Match            98.4%;  Score 2501;  DB 8;  Length 503;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-226;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 7
ADL18672
ID   ADL18672 standard; protein; 503 AA.
XX
AC   ADL18672;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human cytochrome P450 enzyme 3A4 protein.
XX
KW   protein array; protein moiety; drug metabolising enzyme; DME;
KW   drug metabolism; drug toxicity; cytotoxicity; drug metabolite;
KW   metabolic pathway; human; cytochrome; enzyme; P450.
XX
OS   Homo sapiens.
XX
PN   WO2004025244-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-IB005258.
XX
PR   16-SEP-2002; 2002US-0410815P.
PR   05-DEC-2002; 2002US-00313963.
PR   05-DEC-2002; 2002WO-GB005499.
XX
PA   (SENS-) SENSE PROTEOMIC LTD.
XX
PI   Boutell JM,  Godber BLJ,  Hart DJ,  Bockett NA,  Kozlowski R;
XX
DR   WPI; 2004-270121/25.
DR   N-PSDB; ADL18671.
XX
PT   New protein array comprising a surface having spatially defined locations
PT   containing drug metabolizing enzymes, examining gender and ethnicity-
PT   related differences in drug metabolism or cytotoxicity of drug
PT   metabolites.
XX
PS   Example 3; Fig 3B; 72pp; English.
XX
CC   The present invention describes a protein array comprising a surface
CC   having spatially defined locations where at each location there are
CC   deposited at least two protein moieties capable of forming a complex,
CC   where the complex is transiently formed and where the protein moieties
CC   act sequentially on a substrate of interest and are derived from one or
CC   more drug metabolising enzymes (DMEs). Also described: (1) a method of
CC   making a protein array; (2) an array made by the method of (1); (3) a
CC   method of screening a set of protein moieties for molecules which
CC   interact with one or more proteins; (4) a method of simultaneously
CC   determining the relative properties of members of a set of protein
CC   moieties; and (5) a method of expressing and purifying a DME. The protein
CC   array is useful in examining gender differences in drug metabolism,
CC   ethnicity-related differences in drug metabolism and toxicity between two
CC   or more mammalian species, e.g. human and rat and cytotoxicity of drug
CC   metabolites, in defining and quantifying metabolic pathways for small
CC   molecules, in screening of compounds that binds and inhibits individual
CC   DMEs and in analysing induction of P450 expression by one or more
CC   compounds of interest and the effects of mutation on the activity of a
CC   DME of interest. The present sequence represents human cytochrome P450
CC   enzyme 3A4, which is used in the exemplification of the present
CC   invention.
XX
SQ   Sequence 503 AA;

  Query Match            98.4%;  Score 2501;  DB 8;  Length 503;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-226;
  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGPYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503
```

```
RESULT 8
ADD48378
ID   ADD48378 standard; protein; 502 AA.
XX
AC   ADD48378;
XX
DT   02-DEC-2004  (revised)
DT   29-JAN-2004  (first entry)
XX
DE   Human Protein A29815, SEQ ID NO 14079.
XX
KW   Human; pain; neuronal tissue; gene therapy;
KW   spinal segmental nerve injury; chronic constriction injury; CCI;
KW   spared nerve injury; SNI; Chung.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   WO2003016475-A2.
XX
PD   27-FEB-2003.
XX
PF   14-AUG-2002; 2002WO-US025765.
XX
PR   14-AUG-2001; 2001US-0312147P.
PR   01-NOV-2001; 2001US-0346382P.
PR   26-NOV-2001; 2001US-0333347P.
XX
PA   (GEHO ) GEN HOSPITAL CORP.
PA   (FARB ) BAYER AG.
XX
PI   Woolf C,  D'urso D,  Befort K,  Costigan M;
XX
DR   WPI; 2003-268312/26.
DR   GENBANK; A29815.
XX
PT   New composition comprising two or more isolated polypeptides, useful for
PT   preparing a medicament for treating pain in an animal.
XX
PS   Example 1; Page; 1017pp; English.
XX
CC   The invention discloses a composition comprising two or more isolated rat
CC   or human polynucleotides or a polynucleotide which represents a fragment,
CC   derivative or allelic variation of the nucleic acid sequence. Also
CC   claimed are a vector comprising the novel polynucleotide, a host cell
CC   comprising the vector, a method for identifying a nucleotide sequence
CC   which is differentially regulated in an animal subjected to pain and a
CC   kit to perform the method, an array, a method for identifying an agent
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (described in Table 3
CC   of the specification) which is differentially expressed during pain.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 502 AA;

  Query Match             98.1%;  Score 2494;  DB 7;  Length 502;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-225;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 203

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 263

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 323

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 383

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 502
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RESULT 9
AAR72363
ID   AAR72363 standard; protein; 503 AA.
XX
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AC   AAR72363;
XX
DT   25-MAR-2003  (revised)
DT   14-NOV-1995  (first entry)
XX
DE   Human cytochrome P450 molecular species 3A4 protein.
XX
KW   Human cytochrome P450; amplification; PCR; primer; expression vector;
KW   yeast NADPH-P450 reductase; safety; fusion protein; metabolite;
KW   carcinogen; mutagen; liver metabolism.
XX
OS   Homo sapiens.
XX
PN   EP644267-A2.
XX
PD   22-MAR-1995.
XX
PF   20-JUL-1994;   94EP-00111298.
XX
PR   20-JUL-1993;   93JP-00201120.
PR   21-JUL-1993;   93JP-00180246.
PR   30-JUL-1993;   93JP-00208279.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI   Hayashi K,  Sakaki T,  Yabusaki Y,  Komai K,  Kaneko H,  Nakatsuka I;
XX
DR   WPI; 1995-116991/16.
DR   N-PSDB; AAQ87717.
XX
PT   Evaluation of safety of a chemical cpd. - using recombinant yeast
PT   expressing human cytochrome p450 and a yeast NADPH-P450 reductase.
XX
PS   Example; Page 31-33; 124pp; English.
XX
CC   The amino acid sequence of the human cytochrome P450 species 3A4. The
CC   cDNA was amplified by PCR using the primers AAQ87743-6. The product was
CC   cloned into the yeast expression vectors pAAH5N or pAHRR to produce the
CC   vectors p3A4 for the expression of the cytochrome P450 alone or p3A4R for
CC   co-expression with the yeast NADPH-P450 reductase. The vectors are used
CC   in a method for evaluating the safety of a chemical compound by reacting
CC   the chemical compound with recombinantly produced human cytochrome P450
CC   molecular species 1A2 (AAQ87714), 2C9 (AAQ87715), 2E1 (AAQ87716), or 3A4,
CC   or their auxillary species and variants (AAQ87718-32), and yeast NADPH-
CC   P450 reductase, either as a fused protein or in cell extracts, and
CC   analysing the resulting metabolite to assess the safety of the chemical
CC   compound. The method is useful for determining whether the chemical
CC   compound, or its metabolite, will be converted into a carcinogenic or
CC   mutagenic form through metabolism in the liver. (Updated on 25-MAR-2003
CC   to correct PN field.)
XX
SQ   Sequence 503 AA;

  Query Match             98.1%;  Score 2494;  DB 2;  Length 503;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-225;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 10
AAR81464
ID   AAR81464 standard; protein; 503 AA.
XX
AC   AAR81464;
XX
DT   01-AUG-1996  (first entry)
XX
DE   Human derived cytochrome P4503A4.
XX
KW   Human derived cytochrome; P4503A4; commercial cDNA library; yeast;
KW   transfection; recombinant production; expression vector; mammal;
KW   immunisation; sensitisation; antibody; determination; detection;
KW   non-cross reactive.
XX
OS   Homo sapiens.
XX
PN   JP08027197-A.
XX
PD   30-JAN-1996.
XX
PF   13-JUL-1994;   94JP-00161552.
XX
PR   13-JUL-1994;   94JP-00161552.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
DR   WPI; 1996-136338/14.
DR   N-PSDB; AAT17399.
XX
PT   Antibody recognising human derived cytochrome P4502A4 - allows specific
PT   detection of cytochrome P450 species in humans.
XX
PS   Example 1; Page 10-12; 13pp; Japanese.
XX
CC   The present sequence is the human derived cytochrome (HDC) P4503A4, which
CC   was obtd. from a commercial cDNA library. Yeast were transfected with an
CC   expression vector contg. the HDC cDNA, cultured and then disrupted to
CC   give a microsomal fraction. The HDC was purified from the fraction, and
CC   used to immunise and sensitise a mammal. Blood was drawn from the mammal,
CC   and an anti-HDC antibody isolated. The antibody obtd. recognises HDC
CC   P4503A4, partic. at a serum dilution rate of 1:10000, and is
CC   substantially without cross reaction to other HDC P450 spp
XX
SQ   Sequence 503 AA;

  Query Match             98.1%;  Score 2494;  DB 2;  Length 503;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-225;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 11
AAR93170
ID   AAR93170 standard; protein; 503 AA.
XX
AC   AAR93170;
XX
DT   11-OCT-1996  (first entry)
XX
DE   Human cytochrome P450 molecular species 3A4 protein.
XX
KW   Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
KW   liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
KW   evaluation; safety; fusion protein; metabolite; detoxification;
KW   carcinogenic.
XX
OS   Homo sapiens.
XX
PN   JP08056695-A.
XX
PD   05-MAR-1996.
XX
PF   15-JUL-1994;   94JP-00164184.
XX
PR   20-JUL-1993;   93JP-00201120.
PR   30-JUL-1993;   93JP-00208279.
PR   17-JUN-1994;   94JP-00136053.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
DR   WPI; 1996-182311/19.
DR   N-PSDB; AAT28383.
XX
PT   Novel method for the evaluation of the safety of a cpd. - using a human
PT   cytochrome P450 and yeast NADPH reductase to determine whether the
PT   analyte cpd. is detoxified or metabolised to a carcinogen.
XX
PS   Example 1; Page 24-26; 74pp; Japanese.
XX
CC   This is the amino acid sequence of the human cytochrome P450 molecular
CC   species 3A4 protein. The corresp. gene was amplified from a human liver
CC   derived cDNA library as 2 fragments of 0.6 and 0.9 kb using primers
CC   AAT26933-6. The prod. was cloned into the yeast expression vector pAAH5N
CC   to generate plasmid p3A4 for prodn. of the cytochrome only or into the
CC   vector pAHRR to generate the plasmid p3A4R for co-prodn. with the yeast
CC   NADPH-P450 reductase. The sequence is placed under control of the yeast
CC   ADH gene promoter and terminator. The vectors are used in a method for
CC   evaluating the safety of a cpd. by reacting the test cpd. with
CC   recombinantly produced human cytochrome P450 mol. species 1A2 (AAT28380),
CC   2C9 (AAT28381), 2B1 (AAT28382), 3A4 or their variants (AAT28384-98)
CC   together with yeast NADPH-P450 reductase (either as a fused protein or as
CC   a cell extract) and analysing the resultant metabolite. The cpd. is
CC   considered "safe" if it is detoxified or not rendered carcinogenic or
CC   "unsafe" if it is not detoxified or is metabolised to a carcinogenic cpd
XX
SQ   Sequence 503 AA;

  Query Match             98.1%;  Score 2494;  DB 2;  Length 503;
  Best Local Similarity   99.8%;  Pred. No. 2.5e-225;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 12
AAY05202
ID   AAY05202 standard; protein; 503 AA.
XX
AC   AAY05202;
XX
DT   17-JUN-1999  (first entry)
XX
DE   Human CYP3A4 protein.
XX
KW   CYP3A4 gene polymorphism; polymorphic locus; human; altered metabolism;
KW   CYP3A4 substrate; drug-drug interaction identification; toxin exposure;
KW   genetic linkage detection; phenotypic variation.
XX
OS   Homo sapiens.
XX
PN   WO9913106-A1.
XX
PD   18-MAR-1999.
XX
PF   02-SEP-1998;   98WO-US018158.
XX
PR   10-SEP-1997;   97US-0058612P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
```

PI Lichter JB, Guida M;
XX
DR WPI; 1999-215070/18.
DR N-PSDB; AAX28295.
XX
PT New isolated CYP3A4 polymorphic sequences.
XX
PS Disclosure; Page 25-27; 40pp; English.
XX
CC This sequence represents the human CYP3A4 gene protein. The invention
CC relates to a CYP3A4 sequence polymorphism, which is part of a non-
CC naturally occurring chromosome. Nucleic acids comprising the CYP3A4
CC polymorphic sequences can be used to screen patients for altered
CC metabolism for CYP3A4 substrates, potential drug-drug interactions, and
CC adverse/side effects as well as diseases that result from environmental
CC or occupational exposure to toxins. They can also be used to establish
CC animal, cell culture and in vitro cell-free models for drug metabolism.
CC Polymorphic CYP3A4 gene sequences can be used for expression studies to
CC determine the effect of promoter and/or intron sequence variations on
CC mRNA expression and stability. The polymorphisms are also used as single
CC nucleotide polymorphisms to detect genetic linkage to phenotypic
CC variation in activity and expression of CYP3A4. The nucleic acids can
CC also be used to generate genetically modified non-human animals or site
CC specific gene modifications in cell lines
XX
SQ Sequence 503 AA;

Query Match 98.1%; Score 2494; DB 2; Length 503;
Best Local Similarity 99.8%; Pred. No. 2.5e-225;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503
```

RESULT 13
ADQ89978
ID ADQ89978 standard; protein; 503 AA.
XX
AC ADQ89978;
XX
DT 21-OCT-2004 (first entry)
XX
DE Antagonist of cell cycle progression polypeptide #204.
XX
KW Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
OS Homo sapiens.
XX
PN WO2004063362-A2.
XX
PD 29-JUL-2004.
XX
PF 31-DEC-2003; 2003WO-GB005635.
XX
PR 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
PA (CYCL-) CYCLACEL LTD.
XX
PI Glover D, Bell G, Frenz L, Midgley C;
XX
DR WPI; 2004-544089/52.
DR N-PSDB; ADQ89977.
XX
PT New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
PS Claim 2; SEQ ID NO 408; 461pp; English.
XX
CC The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
SQ Sequence 503 AA;

Query Match 98.1%; Score 2494; DB 8; Length 503;
Best Local Similarity 99.8%; Pred. No. 2.5e-225;
Matches 478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPPFLSITVFPPLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 14
ADO47239
ID   ADO47239 standard; protein; 502 AA.
XX
AC   ADO47239;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human cytochrome P450 CYP3A4 SeqID 11.
XX
KW   dynamics docking; cytochrome P450; multispecific enzyme;
KW   protein coordinate data; common structural block; CSB; human.
XX
OS   Homo sapiens.
XX
PN   WO2004038655-A2.
XX
PD   06-MAY-2004.
XX
PF   28-OCT-2003; 2003WO-IB005134.
XX
PR   28-OCT-2002; 2002US-0421569P.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Andre F,  Delaforge M,  Loiseau N;
XX
DR   WPI; 2004-389974/36.
XX
PT   Designing 3 dimensional (3D) protein model, by identifying common
PT   structural blocks (CSBs) among family members, aligning sequence,
PT   defining 3D structure of CSBs, global constraints, selecting rotamers,
PT   determining, optimizing 3D structures.
XX
PS   Claim 14; SEQ ID NO 11; 193pp; English.
XX
CC   This invention relates to a novel method for performing restrained
CC   dynamics docking of one or more substrates on multi-specific enzymes.
CC   Specifically, it refers to determining the three-dimensional structure of
CC   active sites that are flexible and can adapt to different substrates i.e.
CC   multispecific enzymes such as cytochrome P450. The present invention
CC   describes identifying common structural blocks (CSBs) among members of
CC   the family, aligning primary amino acid sequences, aligning the protein
CC   as compared on the first alignment to obtain a second alignment, defining
CC   3D structure of protein CSBs, defining global constraints and selecting
CC   rotamers, in order to determine the family of 3D model protein structures
CC   and optimise models by dihedral angles. Accordingly, the method can be
CC   used for screening, designing or identifying natural, unnatural or
CC   substrate analogues, as well as inhibitors, activators or modulators of
CC   the multispecific enzyme in question. In addition, it can determine the
CC   effect of a first substrate on a second substrate, which can then be
CC   applied to pharmaceutical products. Furthermore, the method can be used
CC   to determine the oxidative modification of the substrate according to its
CC   proximity to a haem molecule, for performing dynamic docking of the
CC   metabolite either in the absence or presence of a second substrate in the
CC   computed simulation and to compare the energy of the bound metabolite
CC   relative to the energy of its parent substrate bound, in order to
CC   determine if the exit of the given metabolite from the enzyme is favoured
CC   or not. This polypeptide sequence is a protein from the cytochrome P450
CC   family of enzymes, given in an exemplification of the invention.
XX
SQ   Sequence 502 AA;

  Query Match            97.0%;  Score 2466;  DB 8;  Length 502;
  Best Local Similarity  99.2%;  Pred. No. 1.1e-222;
  Matches  475;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        144 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 203

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        204 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 263

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        264 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 323

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 PVDQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 383

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        384 GMFIPKGWVVMIPSYALHRDPKYMTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 502


RESULT 15
ADO47238
ID   ADO47238 standard; protein; 503 AA.
XX
AC   ADO47238;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human cytochrome P450 CYP3A3 SeqID 10.
XX
KW   dynamics docking; cytochrome P450; multispecific enzyme;
KW   protein coordinate data; common structural block; CSB; human.
XX
OS   Homo sapiens.
XX
PN   WO2004038655-A2.
XX
PD   06-MAY-2004.
XX
PF   28-OCT-2003; 2003WO-IB005134.
XX
PR   28-OCT-2002; 2002US-0421569P.
XX
PA   (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Andre F,  Delaforge M,  Loiseau N;
XX
DR   WPI; 2004-389974/36.
XX
PT   Designing 3 dimensional (3D) protein model, by identifying common
PT   structural blocks (CSBs) among family members, aligning sequence,
PT   defining 3D structure of CSBs, global constraints, selecting rotamers,
PT   determining, optimizing 3D structures.
XX
PS   Disclosure; SEQ ID NO 10; 193pp; English.
XX
CC   This invention relates to a novel method for performing restrained
```

CC dynamics docking of one or more substrates on multi-specific enzymes.
CC Specifically, it refers to determining the three-dimensional structure of
CC active sites that are flexible and can adapt to different substrates i.e.
CC multispecific enzymes such as cytochrome P450. The present invention
CC describes identifying common structural blocks (CSBs) among members of
CC the family, aligning primary amino acid sequences, aligning the protein
CC as compared on the first alignment to obtain a second alignment, defining
CC 3D structure of protein CSBs, defining global constraints and selecting
CC rotamers, in order to determine the family of 3D model protein structures
CC and optimise models by dihedral angles. Accordingly, the method can be
CC used for screening, designing or identifying natural, unnatural or
CC substrate analogues, as well as inhibitors, activators or modulators of
CC the multispecific enzyme in question. In addition, it can determine the
CC effect of a first substrate on a second substrate, which can then be
CC applied to pharmaceutical products. Furthermore, the method can be used
CC to determine the oxidative modification of the substrate according to its
CC proximity to a haem molecule, for performing dynamic docking of the
CC metabolite either in the absence or presence of a second substrate in the
CC computed simulation and to compare the energy of the bound metabolite
CC relative to the energy of its parent substrate bound, in order to
CC determine if the exit of the given metabolite from the enzyme is favoured
CC or not. This polypeptide sequence is a protein from the cytochrome P450
CC family of enzymes, given in an exemplification of the invention.
XX
SQ Sequence 503 AA;

Query Match 96.4%; Score 2449.5; DB 8; Length 503;
Best Local Similarity 97.9%; Pred. No. 3.8e-221;
Matches 470; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 83

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         84 TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 143

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||| |||||||||||||||||:|||||:||||||||| |
Db        144 MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV 203

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        204 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKAVKRMKESRLEDT 263

Qy        243 QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              |||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||||
Db        264 QKHRVDFLQLMIDSHKNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 323

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        324 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 383

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        384 NGMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 443

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: July 8, 2005, 14:26:00
Job time : 171 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:10:22 ; Search time 41 Seconds
(without alignments)
1138.174 Million cell updates/sec

Title: US-10-690-991-2
Perfect score: 2542
Sequence: 1 MAYGTHSHGLFKKLGIPGPT.....PVVLKVESRDGTVSGAHHHH 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2501	98.4	503	2	A29815	cytochrome P450 3A
2	2449.5	96.4	504	2	A29410	cytochrome P450, g
3	2372	93.3	503	2	S28168	nifedipine oxidase
4	2233	87.8	503	2	JX0062	cytochrome P450 3A
5	2142.5	84.3	502	1	A34101	cytochrome P450 3A
6	2077	81.7	503	2	S14275	steroid 6beta-mono
7	2003	78.8	503	2	JC4702	cytochrome P450 3A
8	1989	78.2	501	2	A34236	cytochrome P450 3A
9	1961	77.1	503	2	S50211	cytochrome P450 3A
10	1957	77.0	503	2	JC7627	cytochrome P450 3A
11	1946.5	76.6	504	2	A22631	cytochrome P450 3A
12	1937	76.2	501	2	A29487	cytochrome P450 3A
13	1935.5	76.1	504	2	A60564	cytochrome P450 3A
14	1904.5	74.9	504	2	A25222	cytochrome P450 3A
15	1902.5	74.8	502	2	JX0334	cytochrome P450 3A
16	1878.5	73.9	504	2	S50892	cytochrome P450 3A
17	1802	70.9	497	2	S52097	cytochrome P450III
18	1788	70.3	503	2	A40843	cytochrome P450 3
19	838.5	33.0	534	2	A41766	thromboxane-A synt
20	837.5	32.9	533	1	S48161	thromboxane-A synt
21	827.5	32.6	533	2	S42404	thromboxane-A synt
22	789.5	31.1	533	2	JN0683	thromboxane-A synt
23	656.5	25.8	460	2	B41766	thromboxane-A synt
24	656	25.8	509	1	A32157	cytochrome P450 6
25	639	25.1	518	2	T24783	hypothetical prote
26	630	24.8	518	2	T20908	hypothetical prote
27	626	24.6	498	1	S48058	cytochrome P450 CY
28	623	24.5	520	2	T24777	hypothetical prote
29	621.5	24.4	507	1	A47198	cytochrome P450 6A
30	620.5	24.4	519	2	T24784	hypothetical prote
31	602.5	23.7	509	2	T24785	hypothetical prote
32	599	23.6	517	2	T20907	hypothetical prote
33	595.5	23.4	503	2	JC5321	cytochrome P450 mo
34	594	23.4	520	2	T24778	hypothetical prote
35	591.5	23.3	518	2	T24779	hypothetical prote
36	590.5	23.2	510	2	T19763	hypothetical prote
37	588.5	23.2	522	2	T19762	hypothetical prote
38	587	23.1	520	2	T24780	hypothetical prote
39	556.5	21.9	515	2	T24781	hypothetical prote
40	543.5	21.4	496	1	S41192	cytochrome P450 4D
41	530.5	20.9	513	2	JC7120	cytochrome P450 en
42	529	20.8	494	2	JC5320	cytochrome P450 mo
43	528.5	20.8	544	2	T27750	hypothetical prote
44	520.5	20.5	501	2	T19766	hypothetical prote
45	520	20.5	475	2	A88414	protein C36A4.3 [i

ALIGNMENTS

RESULT 1
A29815
cytochrome P450 3A4 nifedipine oxidase (EC 1.14.14.-) - human
N;Alternate names: cytochrome P450(PCN1); cytochrome P450-HM1
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A29815; S16900; A25517; A32199; PX0012; S03851
R;Gonzalez, F.J.; Schmid, B.J.; Umeno, M.; McBride, O.W.; Hardwick, J.P.; Meyer, U.A.;
DNA 7, 79-86, 1988
A;Title: Human P450PCN1: sequence, chromosome localization, and direct evidence through
A;Reference number: A29815; MUID:88195781; PMID:3267210
A;Accession: A29815
A;Molecule type: mRNA
A;Residues: 1-503 <GON>
A;Cross-references: UNIPROT:P08684; GB:M18907; NID:g181373; PIDN:AAA35745.1; PID:g18137
R;Spurr, N.K.; Gough, A.C.; Stevenson, K.; Wolf, C.R.
Hum. Genet. 81, 171-174, 1989
A;Title: The human cytochrome P450 CYP3 locus: assignment to chromosome 7q22-qter.
A;Reference number: S16900; MUID:89108438; PMID:2563251
A;Accession: S16900
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-391,'W',393-503 <SP2>
A;Cross-references: EMBL:X12387; NID:g35910; PIDN:CAA30944.1; PID:g35911
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1988
R;Beaune, P.H.; Umbenhauer, D.R.; Bork, R.W.; Lloyd, R.S.; Guengerich, F.P.
Proc. Natl. Acad. Sci. U.S.A. 83, 8064-8068, 1986
A;Title: Isolation and sequence determination of a cDNA clone related to human cytochro
A;Reference number: A25517; MUID:87041402; PMID:3464943
A;Accession: A25517
A;Molecule type: mRNA
A;Residues: 1-391,'W',393-503 <BEA>
R;Bork, R.W.; Muto, T.; Beaune, P.H.; Srivastava, P.K.; Lloyd, R.S.; Guengerich, F.P.
J. Biol. Chem. 264, 910-919, 1989
A;Title: Characterization of mRNA species related to human liver cytochrome P-450 nifed
A;Reference number: A32199; MUID:89093163; PMID:2463251
A;Accession: A32199
A;Molecule type: protein
A;Residues: 'X',2-9,'XXX',13-15 <BOR>
R;Komori, M.; Hashizume, T.; Ohi, H.; Miura, T.; Kitada, M.; Nagashima, K.; Kamataki, T
J. Biochem. 104, 912-916, 1988
A;Title: Cytochrome P-450 in human liver microsomes: high-performance liquid chromatogr
A;Reference number: PX0012; MUID:89214010; PMID:3243766
A;Accession: PX0012
A;Molecule type: protein
A;Residues: 'X',2-11,'X',13-25 <KOM>
A;Experimental source: liver microsome
C;Genetics:
A;Gene: GDB:CYP3A4
A;Cross-references: GDB:118782
A;Map position: 7q22.1-7q22.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology

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C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F;302-464/Domain: cytochrome P450 homology <P45>
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             98.4%;  Score 2501;  DB 2;  Length 503;
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  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 2
A29410
cytochrome P450, glucocorticoid-inducible, hepatic - human
N;Alternate names: cytochrome P450 3A3; cytochrome P450 HLp
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A29410; A25170; A25450
R;Molowa, D.T.; Schuetz, E.G.; Wrighton, S.A.; Watkins, P.B.; Kremers, P.; Mendez-Picon,
Proc. Natl. Acad. Sci. U.S.A. 83, 5311-5315, 1986
A;Title: Complete cDNA sequence of a cytochrome P-450 inducible by glucocorticoids in hu
A;Reference number: A94111; MUID:86259780; PMID:3460094
A;Accession: A29410
A;Molecule type: mRNA
A;Residues: 1-504 <MOL>
A;Cross-references: UNIPROT:P05184; GB:M13785; NID:g181353; PIDN:AAA35742.1; PID:g181354
R;Watkins, P.B.; Wrighton, S.A.; Maurel, P.; Schuetz, E.G.; Mendez-Picon, G.; Parker, G.
Proc. Natl. Acad. Sci. U.S.A. 82, 6310-6314, 1985
A;Title: Identification of an inducible form of cytochrome P-450 in human liver.
A;Reference number: A25170; MUID:85298342; PMID:3898085
A;Accession: A25170
A;Molecule type: protein
A;Residues: 2-21 <WAT>
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; liver; metalloprotein; monooxy
F;303-465/Domain: cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             96.4%;  Score 2449.5;  DB 2;  Length 504;
  Best Local Similarity   97.9%;  Pred. No. 2.6e-175;
  Matches  470;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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Db         85 TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKAVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSHKNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
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Db        385 NGMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        445 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 504


RESULT 3
S28168
nifedipine oxidase (EC 1.14.14.-) cytochrome P450 3A8 - crab-eating macaque
N;Alternate names: cytochrome P450 CMLc; cytochrome P450 MKnf2; cytochrome P450-MK2
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 09-Jul-2004
C;Accession: S28168; S04509; S36875
R;Komori, M.; Kikuchi, O.; Sakuma, T.; Funaki, J.; Kitada, M.; Kamataki, T.
Biochim. Biophys. Acta 1171, 141-146, 1992
A;Title: Molecular cloning of monkey liver cytochrome P-450 cDNAs: similarity of the pri
A;Reference number: S28166; MUID:93129612; PMID:1282830
A;Accession: S28168
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-503 <KOM>
A;Cross-references: UNIPROT:P33268; GB:S53047; NID:g263692; PIDN:AAB24952.1; PID:g263693
R;Ohta, K.; Kitada, M.; Hashizume, T.; Komori, M.; Ohi, H.; Kamataki, T.
Biochim. Biophys. Acta 996, 142-145, 1989
A;Title: Purification of cytochrome P-450 from polychlorinated biphenyl-treated crab-eat
A;Reference number: S04509; MUID:89287352; PMID:2500151
A;Accession: S04509
A;Molecule type: protein
A;Residues: 1-22 <OHT>
R;Ohmori, S.; Horie, T.; Guengerich, F.P.; Kiuchi, M.; Kitada, M.
Arch. Biochem. Biophys. 305, 405-413, 1993
A;Title: Purification and characterization of two forms of hepatic microsomal cytochrome
A;Reference number: S36874; MUID:93384294; PMID:8373178
A;Accession: S36875
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <OHM>
C;Genetics:
A;Gene: CYP3A8
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F;302-464/Domain: cytochrome P450 homology <P45>
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             93.3%;  Score 2372;  DB 2;  Length 503;
  Best Local Similarity   93.9%;  Pred. No. 1.6e-169;
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Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         25 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGFWTFDMECYKKYGKVWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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Db         85 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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Db        145 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||||||||||||||:|||:|||||||||  :||||||:|||||||:|||||:||
Db        205 ENTKKLLRFDFLDPFFLSITIFPFIIPILEVLNISIFPREVTSFLRKSVKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
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Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
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Db        325 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMVVNETLRIFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||||| ||||| |||||||||||||| ||||||||||||||||||||
Db        385 GIFIPKGVVVMIPSYALHHDPKYWPEPEKFLPERFSKKNNDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        445 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 503
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RESULT 4
JX0062
cytochrome P450 3A7 - human
N;Alternate names: cytochrome P450 3A3; cytochrome P450 HFL33; cytochrome P450 HLp2; cyt
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JX0062; PX0014; S04983; S02152
R;Komori, M.; Nishio, K.; Ohi, H.; Kitada, M.; Kamataki, T.
J. Biochem. 105, 161-163, 1989
A;Title: Molecular cloning and sequence analysis of cDNA containing the entire coding re
A;Reference number: JX0062; MUID:89255154; PMID:2722762
A;Accession: JX0062
A;Molecule type: mRNA
A;Residues: 1-503 <KOM>
A;Cross-references: UNIPROT:P24462; GB:D00408; NID:g220148; PIDN:BAA00310.1; PID:g220149
A;Experimental source: fetal liver
R;Komori, M.; Hashizume, T.; Ohi, H.; Miura, T.; Kitada, M.; Nagashima, K.; Kamataki, T.
J. Biochem. 104, 912-916, 1988
A;Title: Cytochrome P-450 in human liver microsomes: high-performance liquid chromatogra
A;Reference number: PX0012; MUID:89214010; PMID:3243766
A;Accession: PX0014
A;Molecule type: protein
A;Residues: 1-25 <KO2>
A;Experimental source: liver microsome
R;Komori, M.; Nishio, K.; Fujitani, T.; Ohi, H.; Kitada, M.; Mima, S.; Itahashi, K.; Kam
Arch. Biochem. Biophys. 272, 219-225, 1989
A;Title: Isolation of a new human fetal liver cytochrome P450 cDNA clone: evidence for e
A;Reference number: S04983; MUID:89286124; PMID:2786707
A;Accession: S04983
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 282-503 <KO3>
R;Wrighton, S.A.; Vandenbranden, M.
Arch. Biochem. Biophys. 268, 144-151, 1989
A;Title: Isolation and characterization of human fetal liver cytochrome P450HLp2: a thir
A;Reference number: S02152; MUID:89104413; PMID:2492179
A;Accession: S02152
A;Molecule type: protein
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A;Gene: GDB:CYP3A7
A;Cross-references: GDB:134409
A;Map position: 7q22.1-7q22.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metall
F;302-464/Domain: cytochrome P450 homology <P45>
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 87.8%; Score 2233; DB 2; Length 503;
Best Local Similarity 88.7%; Pred. No. 3.9e-159;
Matches 425; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
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Db         25 YGTRTHGLFKKLGIPGPTPLPFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPMLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||||||||||||||:||||||||||||:|||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||||||||||||||| ||||||||||||||||:||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||||: |||| ||| ||||| |||| ||| |||:| :|| |||||::|| ||::|
Db        205 ENTKKLLRFNPLDPFVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKET 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||||||||::|:|||||||||:||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKDSETHKALSDLELMAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||:|:||| ||||||||||||||:||||||||||||||:||||||||||||||||
Db        325 PDVQQKVQKEIDTVLPNKAPPTYDTVLQLEYLDMVVNETLRLFPVAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||:||||||:|||||||||||||||||||  ||||  |||:||| |||| |||||
Db        445 MRFALVNMKLALVRVLQNFSFKPCKETQIPLKLRFGGLLLTEKPIVLKAESRDETVSGA 503
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RESULT 5
A34101
cytochrome P450 3A5 - human
N;Alternate names: cytochrome P450 HLp2
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34101; S06491; I52302
R;Aoyama, T.; Yamano, S.; Waxman, D.J.; Lapenson, D.P.; Meyer, U.A.; Fischer, V.; Tyndal
J. Biol. Chem. 264, 10388-10395, 1989
A;Title: Cytochrome P-450 hPCN3, a novel cytochrome P-450 IIIA gene product that is dif
DNA-expressed hPCN1 and hPCN3 for the metabolism of steroid hormones and cyclosporine.
A;Reference number: A34101; MUID:89278095; PMID:2732228
A;Accession: A34101
A;Molecule type: mRNA
A;Residues: 1-502 <AOY>
A;Cross-references: UNIPROT:P20815; GB:J04813; NID:g181345; PIDN:AAA02993.1; PID:g18134
R;Schuetz, J.D.; Molowa, D.T.; Guzelian, P.S.
Arch. Biochem. Biophys. 274, 355-365, 1989
A;Title: Characterization of a cDNA encoding a new member of the glucocorticoid-respons
A;Reference number: S06491; MUID:90025114; PMID:2802615
A;Accession: S06491
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-304,'P',306-317,'F',319-323,'D',325-376,'G',378-502 <SCH>

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R;Jounaidi, Y.; Guzelian, P.S.; Maurel, P.; Vilarem, M.J.
Biochem. Biophys. Res. Commun. 205, 1741-1747, 1994
A;Title: Sequence of the 5'-flanking region of CYP3A5: comparative analysis with CYP3A4
A;Reference number: I52302; MUID:95110318; PMID:7811260
A;Accession: I52302
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <RES>
A;Cross-references: GB:S74699; NID:g786472; PIDN:AAD14157.1; PID:g4261857
C;Genetics:
A;Gene: GDB:CYP3A5
A;Cross-references: GDB:118783
A;Map position: 7q22.1-7q22.1
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;302-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             84.3%;  Score 2142.5;  DB 1;  Length 502;
  Best Local Similarity   84.1%;  Pred. No. 2.3e-152;
  Matches  402;  Conservative   37;  Mismatches   38;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| :|||||:|||||||||| |||:||| :|   || ||:|||||:|| |:|| |||||
Db         25 YGTRTHGLFKRLGIPGPTPLPLLGNVLSYRQGLWKFDTECYKKYGKMWGTYEGQLPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||:|:||||||||||||||  ||||||||||:||||||||:||||||||||||||||
Db         85 TDPDVIRTVLVKECYSVFTNRRSLGPVGFMKSAISLAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | |||||||||||||||||| ||||||||:|||||||||| ||||||||||||||||||
Db        145 MFPIIAQYGDVLVRNLRREAEKGKPVTLKDIFGAYSMDVITGTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPPFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |:||| |:| |||| |||| :|||| |: | ||: :||::  ||| ||| |||:||| |
Db        205 ESTKKFLKFGFLDLPFLSIILFPFLTPVFEALNVSLFPKDTINFLSKSVNRMKKSRLNDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||:|||||||||||||||||||||| ||||||||||||||||| :||||||
Db        265 QKHRLDFLQLMIDSQNSKETESHKALSDLELAAQSIIFIFAGYETTSSVLSFTLYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||:|||||||||||||| |:||||||||||||||:|:|||| ||||||||
Db        325 PDVQQKLQKEIDAVLPNKAPPTYDAVVQMEYLDMVVNETLRLFPVAIRLERTCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| :|:||:|||| |||||||||:| ||||||| ||:||||||||||:|||||||
Db        385 GVFIPKGSMVVIPTYALHHDPKYWTEPEEFRPERFSKK-KDSIDPYIYTPFGTGPRNCIG 443

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||||||||||||||||||||||||||||||   ||||||||:||||:|||||:||
Db        444 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLDTQGLLQPEKPIVLKVDSRDGTLSG 501


RESULT 6
S14275
steroid 6beta-monooxygenase (EC 1.14.14.-) cytochrome P450 3A - dog
N;Alternate names: steroid 6beta hydroxylase
C;Species: Canis lupus familiaris (dog)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 09-Jul-2004
C;Accession: S14275
R;Ciaccio, P.J.; Graves, P.E.; Bourque, D.P.; Glinsmann-Gibson, B.; Halpert, J.R.
Biochim. Biophys. Acta 1088, 319-322, 1991
A;Title: cDNA and deduced amino acid sequences of a dog liver cytochrome P-450 of the II
A;Reference number: S14275; MUID:91159488; PMID:2001406
A;Accession: S14275
A;Molecule type: mRNA
A;Residues: 1-503 <CIA>
A;Cross-references: UNIPROT:P24463; EMBL:X54915; NID:g909; PIDN:CAA38687.1; PID:g910
C;Genetics:
A;Gene: CYP3A
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metallo
F;302-464/Domain: cytochrome P450 homology <P45>
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             81.7%;  Score 2077;  DB 2;  Length 503;
  Best Local Similarity   79.7%;  Pred. No. 1.8e-147;
  Matches  382;  Conservative   55;  Mismatches   42;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||::||:|:|||||||||||:|  | |  || :|||:|  |||::|||||:||||||
Db         25 YGTYTHGIFRKLGIPGPTPLPFVGTALGYRNGFYVFDMKCFSKYGRMWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||  ||||||||||::||||||:|:||||||:|||||
Db         85 TDPDMIKTVLVKECYSVFTNRRTLGPVGFMKSAISLSEDEEWKRMRTLLSPTFTTGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              | ||| ||||||| |||:||| || : |||||||||||||||||||||||:||||||
Db        145 MFPIIGQYGDVLVNNLRKEAEKGKAINLKDVFGAYSMDVITSTSFGVNIDSLNHPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||:|||||||| || :|||| |: |:||| :||::||:| ||||:|||||||:|
Db        205 ENTKKLLKFDFLDPFFFSILLFPFLTPVFEILNIWLFPKKVTDFFRKSVERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||:|||||| ::|||||||||||||||||||||||||||: |||:|||||||
Db        265 QKHRVDFLQLMINSQNSKEMDTHKALSDLELVAQSIIFIFAGYETTSTSLSFLMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||:|||| |||| |||| ::|||||||:|||||:||| ||||||||||:
Db        325 PDVQQKLQEEIDATFPNKALPTYDALVQMEYLDMVLNETLRLYPIAGRLERVCKKDVEIS 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:||||| |||:|:: |||| | |||:| |||||:||||:|:|| | |||:|||||||
Db        385 GVFIPKGTVVMVPTFTLHRDQSLWPEPEEFRPERFSRKNKDSINPYTYLPFGTGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||:|||||||:||||||||||||||||:  |::|||||:||||| |||:|:||
Db        445 MRFAIMNMKLALVRVLQNFSFKPCKETQIPLKLNAQGIIQPEKPIVLKVEPRDGSVNGA 503


RESULT 7
JC4702
cytochrome P450 3A9 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: JC4702
R;Wang, H.; Kawashima, H.; Strobel, H.W.
Biochem. Biophys. Res. Commun. 221, 157-162, 1996
A;Title: cDNA cloning of a novel CYP3A from rat brain.
A;Reference number: JC4702; MUID:96220175; PMID:8660328
A;Accession: JC4702
A;Molecule type: mRNA
A;Residues: 1-503 <WAN>
A;Cross-references: UNIPROT:P51538; GB:U46118; NID:g1276917; PIDN:AAC52582.1; PID:g12769
C;Comment: This protein is involved in imipramine metabolism. It catalyzes the demethyla
C;Genetics:
A;Gene: cyp3a9
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; transmembrane protein
F;302-464/Domain: cytochrome P450 homology <P45>
F;435-453/Region: HR2 region
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             78.8%;  Score 2003;  DB 2;  Length 503;
  Best Local Similarity   76.6%;  Pred. No. 6.2e-142;
  Matches  367;  Conservative   61;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||:||||||||| |||||| ||:| |||  ||  |||||||:|| |||:||||||
Db         25 YGTHSHGIFKKLGIPGPKPLPFLGTILAYRKGFWEFDKYCHKKYGKLWGLYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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                |||||:||||||||||| ||||| ||||| :| ||||:|||||||:|:||||||||||||||
Db          85 TDPDIIKTVLVKECYSTFTNRRNFGPVGILKKAISISEDEEWKRIRALLSPTFTSGKLKE 144

Qy         123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
                | ||| || |:||||:|: :| ||| ::||:|||||||||:|||||:|||||||||||
Db         145 MFPIINQYTDMLVRNMRQGSEEGKPTSMKDIFGAYSMDVITATSFGVNVDSLNNPQDPFV 204

Qy         183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
                |  ||||:||  || |||:|:|||| |: | ||: :|||:| :| : ||:||||:|:::
Db         205 EKVKKLLKFDIFDPLFLSVTLFPFLTPLFEALNVSMFPRDVIDFFKTSVERMKENRMKEK 264

Qy         243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
               :| |:||||||:|||||  :|||||||:|:||||:||||||||||||| |||::| || |
Db         265 EKQRMDFLQLMINSQNSKVKDSHKALSDVEIVAQSVIFIFAGYETTSSALSFVLYLLAIH 324

Qy         303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
               ||:|:|||:|||| |||||  ||||:|||||||||||||||:||| ||||||| |||||
Db         325 PDIQKKLQDEIDAALPNKAHATYDTLLQMEYLDMVVNETLRLYPIAGRLERVCKTDVEIN 384

Qy         363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERPSKKNKDNIDPYIYTPFGSGPRNCIG 422
               |:||||| |||||::|||:|| || |||:| ||||||||:|||:||:| |||:|||||||
Db         385 GVFIPKGTVVMIPTFALHKDPHYWPEPEEFRPERFSKKNQDNINPYMYLPFGNGPRNCIG 444

Qy         423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
               |||||||||:||:||||||||:|||||||||||||  ||||||||::||| ||| ||:||
Db         445 MRFALMNMKVALVRVLQNFSFQPCKETQIPLKLSKQGLLQPEKPLLLKVVSRDETVNGA 503


RESULT 8
A34236
cytochrome P450 3A6 (version 2) - rabbit
N;Alternate names: cytochrome P450 3c
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: A34236
R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
J. Biol. Chem. 264, 16222-16228, 1989
A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and
A;Reference number: A34236; MUID:89380226; PMID:2777787
A;Accession: A34236
A;Molecule type: mRNA
A;Residues: 1-501 <POT>
A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
C;Genetics:
A;Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;300-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             78.2%;  Score 1989;  DB 2;  Length 501;
  Best Local Similarity   76.0%;  Pred. No. 6.9e-141;
  Matches  364;  Conservative   64;  Mismatches   51;  Indels    0;  Gaps    0;

Qy           3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
                ||| :|||||:|||||||||||:|| || | ||   ||:|| ||||||:|| :||:||:: |
Db          23 YGTSTHGLFKKMGIPGPTPLPFIGTILEYRKGIWDFDIECRKKYGKMWGLFDGRQPLMVI 82

Qy          63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               |||||||||||||||||||||| |||||||| |:||:|||:|||:|:|||||||||||||
Db          83 TDPDMIKTVLVKECYSVFTNRRSFGPVGFMKKAVSISEDEDWKRVRTLLSPTFTSGKLKE 142

Qy         123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
               |:|||||||||:|||:||| |||| ||::|||||||||| |||||||||| |||||||
Db         143 MLPIIAQYGDVLVKNLRQEAEKGKPVDLKEIFGAYSMDVITGTSFGVNIDSLRNPQDPFV 202

Qy         183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
               :| ::||:| | ||  ||||:|||| || | |:| :||::| :||: ||:::|: ||:|
Db         203 KNVRRLLKFSFFDPLLLSITLFPFLTPIFEALHISMFPKDVMDFLKTSVEKIKDDRLKDK 262

Qy         243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
               || |||||||||:|||||| :|||||  |:|:|||||| :|||||||||  |||||: ||||

Db         263 QKRRVDFLQLMINSQNSKEIDSHKALDDIEVVAQSIIILFAGYETTSSTLSFIMHLLATH 322

Qy         303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
               |||||||||||| :||||   ||||:::|||||||||||||:||| ||||||||||:||
Db         323 PDVQQKLQEEIDTLLPNKELATYDTLVKMEYLDMVVNETLRLYPIAGRLERVCKKDVDIN 382

Qy         363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
               | ||||| :||:|:|||||||::||||::| ||||||||||||:|||| |||:|||||:|
Db         383 GTFIPKGTIVMMPTYALHRDPQHWTEPDEFRPERFSKKNKDNINPYIYHPFGAGPRNCLG 442

Qy         423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
               |||||||:||||:|::|||||| |||||:|||| |||||||||:|||| |||| : ||
Db         443 MRFALMNIKLALVRLMQNFSFKLCKETQVPLKLGKQGLLQPEKPIVLKVVSRDGIIRGA 501


RESULT 9
S50211
cytochrome P450 3A13 - mouse
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S50211; S18155
R;Yanagimoto, T.; Itoh, S.; Sawada, M.; Hashimoto, H.; Kamataki, T.
Biochim. Biophys. Acta 1201, 405-410, 1994
A;Title: Molecular cloning and functional expression of a mouse cytochrome P-450 (Cyp3a
A;Reference number: S50211; MUID:95101705; PMID:7803471
A;Accession: S50211
A;Molecule type: mRNA
A;Residues: 1-503 <YAN>
A;Cross-references: UNIPROT:Q64464; EMBL:X63023; NID:g50634; PIDN:CAA44754.1; PID:g5063
C;Genetics:
A;Gene: CYP3A13
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metall
F;302-464/Domain: cytochrome P450 homology <P45>
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             77.1%;  Score 1961;  DB 2;  Length 503;
  Best Local Similarity   75.7%;  Pred. No. 8.6e-139;
  Matches  361;  Conservative   61;  Mismatches   55;  Indels    0;  Gaps    0;

Qy           3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
                |||||||:|||||||| |||||| ||:| |||    |::|||||||:|| |||:||||||
Db          25 YGTHSHGIFKKLGIPGPKPLPFLGTILAYQKGFWECDIQCHKKYGKMWGLYDGRQPVLAI 84

Qy          63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               ||||:|||||||||| ||||| ||||| :| ||||:|:|||||:|:|||||||||:|||
Db          85 TDPDIIKTVLVKECYSTFTNRRRFGPVGILKKAISISENEEWKRIRALLSPTFTSGRLKE 144

Qy         123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
               | ||| |: |||||:|:    ||| ::||:|||||||||:|||||||||||||||||||
Db         145 MFPIINQFTDVLVRNMRQGLGEGKPTSMKDIFGAYSMDVITATSFGVNIDSLNNPQDPFV 204

Qy         183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
               |  ||||:||  || |||:|:|||| |: : ||: :|||:| :|   ||:||||:|:::
Db         205 EKIKKLLKFDIFDPLFLSVTLFPFLTPVFDALNVSLFPRDVISFFTTSVERMKENRMKEK 264

Qy         243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
               :| |||||||||:||| |  |||||||:|:||||:|||||||||||| ||| :| || |
Db         265 EKQRVDFLQLMINSQNYKTKESHKALSDVEIVAQSVIFIFAGYETTSSALSFALYLLAIH 324

Qy         303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
               ||||:|||:|||| |||||| ||||:||||||||||||||:||| ||||||| |||||
Db         325 PDVQKKLQDEIDAALPNKAPATYDTLLQMEYLDMVVNETLRLYPIAGRLERVCKTDVEIN 384

Qy         363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
               |:|||||:|||:|||||: :|||||:|||||  ||||||  |::||| ||| |||
Db         385 GLFIPKGTVVMIPTFALHKDPKYWPEPEEFRPERFSKKNQDSINPYMYLPFGSGPRNCIG 444

Qy         423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVS 479
               |||||:|||:||:|||||: :|||||:|||||  ||||||  |::||| ||| |||
Db         445 MRFALINMKVALVRVLQNFTVQPCKETEIPLKLSKQGLLQPENPLLLKVVSRDETVS 501
```

RESULT 10
JC7627
cytochrome P450 3A isoform, CYP3A43 protein - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7627
R;Westlind, A.; Malmebo, S.; Johansson, I.; Otter, C.; Andersson, T.B.; Ingelman-Sundber
Biochem. Biophys. Res. Commun. 281, 1349-1355, 2001
A;Title: Cloning and tissue distribution of a novel human cytochrome P450 of the CYP3A s
A;Reference number: JC7627; MUID:21139777; PMID:11243885
A;Accession: JC7627
A;Molecule type: mRNA
A;Residues: 1-503 <WES>
A;Cross-references: UNIPROT:Q9HB55; GB:AF337813
C;Comment: This CYP3A43 protein has broad and overlapping substrate specificities, and a
C;Genetics:
A;Gene: cyp3a43
A;Introns: 24/2; 55/3; 73/2; 106/3; 144/3; 174/2; 224/1; 266/3; 289/1; 342/3; 418/2; 472
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;442/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 77.0%; Score 1957; DB 2; Length 503;
Best Local Similarity 76.2%; Pred. No. 1.7e-138;
Matches 364; Conservative 51; Mismatches 63; Indels 0; Gaps 0;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               |||||||||||||||||: | ||:||:|||:| ||||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | |||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||| ||| ::|||||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:|||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||| |:|||:|| |||||||||||||||||    :||||||:||||  |||  ||
Db        445 MRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 502
```

RESULT 11
A22631
cytochrome P450 3A1, pregnenolone 16-alpha-carbonitrile-inducible - rat
N;Alternate names: testosterone 6beta-hydroxylase
N;Contains: unspecific monooxygenase (EC 1.14.14.1) cytochrome P450 PCN1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Aug-1987 #sequence_revision 29-Aug-1987 #text_change 09-Jul-2004
C;Accession: A22631; PX0035; S21697; S36137; S27107; S30378; I59218
R;Gonzalez, F.J.; Nebert, D.W.; Hardwick, J.P.; Kasper, C.B.
J. Biol. Chem. 260, 7435-7441, 1985
A;Title: Complete cDNA and protein sequence of a pregnenolone 16-alpha-carbonitrile-indu
A;Reference number: A22631; MUID:85207783; PMID:3838989
A;Accession: A22631
A;Molecule type: mRNA
A;Residues: 1-504 <GON>
A;Cross-references: UNIPROT:P04800; GB:M10161; NID:g203777; PIDN:AAA41035.1; PID:g203778
R;Nagata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
A;Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A;Reference number: PX0032; MUID:90375438; PMID:2398038
A;Accession: PX0035
A;Molecule type: protein
A;Residues: 1-26 <NAG>
A;Experimental source: liver, Sprague-Dawley male rat
R;Lechner, M.C.
submitted to the EMBL Data Library, December 1991
A;Reference number: S21697
A;Accession: S21697
A;Molecule type: mRNA
A;Residues: 1-206,'A',208-212,'I',214-231,'V',233-504 <LEC>
A;Cross-references: EMBL:X64401; NID:g56038; PIDN:CAA45743.1; PID:g56039
R;Ribeiro, V.; Lechner, M.C.
Arch. Biochem. Biophys. 293, 147-152, 1992
A;Title: Cloning and characterization of a novel CYP3A1 allelic variant: Analysis of CYP
A;Reference number: S36137; MUID:92117688; PMID:1731631
A;Accession: S36137
A;Molecule type: mRNA
A;Residues: 205-206,'A',208-212,'I',214-231,'V',233-234 <RIB>
A;Cross-references: EMBL:X64401
R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A;Reference number: S27107; MUID:93037516; PMID:1417000
A;Accession: S27107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-24 <TEL>
A;Cross-references: EMBL:X62086
R;Cooper, K.O.; Reik, L.M.; Jayyosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R
Arch. Biochem. Biophys. 301, 345-354, 1993
A;Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A;Reference number: S30378; MUID:93213168; PMID:7681660
A;Accession: S30378
A;Molecule type: protein
A;Residues: 1-25 <COO>
R;Burger, H.
Proc. Natl. Acad. Sci. U.S.A. 89, 2145-2149, 1992
A;Title: Paradoxical transcriptional activation of rat liver cytochrome P-450 3A1 by dex
to primary monolayer cultures of adult rat hepatocytes.
A;Reference number: I59218; MUID:92196074; PMID:1372436
A;Accession: I59218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-24 <BUR>
A;Cross-references: GB:M86850; NID:g205919; PIDN:AAA41780.1; PID:g205920
C;Genetics:
A;Gene: CYP3A1; P450p
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase,
F;303-465/Domain: cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 76.6%; Score 1946.5; DB 2; Length 504;
Best Local Similarity 74.0%; Pred. No. 1e-137;
Matches 355; Conservative 62; Mismatches 62; Indels 1; Gaps 1;

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Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              :|| :|||||| ||||| |||| | :|:|: |   ||:|||||||:|| :||| |: ||
Db         25 FGTRTHGLFKKQGIPGPKPLPFFGTVLNYYMGLWKFDVECHKKYGKIWGLFDGQMPLFAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
               || :||| ||||||:||||||| ||||| |  |:|:|:|||||| |:|||||||||:|||
Db         85 TDTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
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Db        145 MFPIIEQYGDILVKYLKQEAETGKPVTMKKVFGAYSMDVITSTSFGVNVDSLNNPKDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242

Db        205 EKTKKLLRFDFFDPLFLSVVLFPFLTPIYEMLNICMFPKDSIEFFKKFVYRMKETRLDSV 264

Qy        243 QKHRVDFLQLMIDSQN-SKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301

Db        265 QKHRVDFLQLMMNAHNDSKDKESHTALSDMEITAQSIIFIFAGYEPTSSTLSFVLHSLAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361

Db        325 HPDTQKKLQEEIDRALPNKAPPTYDTVMEMEYLDMVLNETLRLYPIGNRLERVCKKDVEI 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421

Db        385 NGVFMPKGSVVMIPSYALHRDPQHWPEPEEFRPERFSKENKGSIDPYVYLPFGNGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481

Db        445 GMRFALMNMKLALTKVLQNFSFQPCKETQIPLKLSRQGLLQPTKPIILKVVPRDEIITGS 504


RESULT 12
A29487
cytochrome P450 3A6 (version 1) - rabbit
N;Alternate names: cytochrome P450 3c
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29487
R;Dalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
DNA 7, 39-46, 1988
A;Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species w
A;Reference number: A29487; MUID:88166352; PMID:3349903
A;Accession: A29487
A;Molecule type: mRNA
A;Residues: 1-501 <DAL>
A;Cross-references: UNIPROT:P11707; GB:M19139; NID:g165573; PIDN:AAA31430.1; PID:g165574
C;Genetics:
A;Gene: CYP3A6
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;301-462/Domain: cytochrome P450 homology <P45>
F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match            76.2%;  Score 1937;  DB 2;  Length 501;
  Best Local Similarity  74.8%;  Pred. No. 5.3e-137;
  Matches  359;  Conservative   63;  Mismatches   56;  Indels    2;  Gaps    2;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCM-FDMECHKKYGKVWGFYDGQQPVLA 61

Db         23 YGTSTHGLFKKMGIPGPTPLPFIGTILEYRKVINWDFDIECRKKYGKMWGLFDGRQPLMV 82

Qy         62 ITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLK 121

Db         83 ITDPDMIKTVLVKECYSVFTNRRSFGPVGFMKKAVSISEDEDWKRVRTLLSPTFTSGKLK 142

Qy        122 EMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPF 181

Db        143 EMLPIIAQYGDVLVKNLRQEAEKASPSTLKEIFGAYSMDVITGTSFGVNIDSLRNPQDPF 202

Qy        182 VENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLED 241

Db        203 VKNVRRLLKFSFFDPLLLSITLFPFLTPIFEALHISMFPKDVMDFLKTSVEKIKDDRLKD 262

Qy        242 TQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301

Db        263 KQKRRVDFLQLMINSQNSKEIDSHKALDDIEVVAQSIIILFAGYETTSSTLSFIMHLLAT 322

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361

Db        323 HPDVQQKLQEEIDTLLPNKELATYDTLVKMEYLDMVVNETLRLYPIAGRLERVCKKDVDI 382

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421

Db        383 NGTFIPKGTIVM-PTYALHRDPQHWTEPDEFRPERFSKKNKDNINPYIYHPFGAGPRNCL 441

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481

Db        442 GMRFALMNIKLALVRLMQNFSFKLCKETQVPLKLGKQGLLQPEKPIVLKVVSESGIIRGA 501


RESULT 13
A60564
cytochrome P450 3A11 - mouse
N;Alternate names: cytochrome P450 3A-UT; cytochrome P450 IIIAM1
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S22334; A60564
R;Yanagimoto, T.; Itoh, S.; Muller-Enoch, D.; Kamataki, T.
Biochim. Biophys. Acta 1130, 329-332, 1992
A;Title: Mouse liver cytochrome P-450 (P-450IIIAM1): its cDNA cloning and inducibility
A;Reference number: S22334; MUID:92223116; PMID:1339292
A;Accession: S22334
A;Molecule type: mRNA
A;Residues: 1-504 <YAN>
A;Cross-references: UNIPROT:Q64459; EMBL:X60452; NID:g50534; PIDN:CAA42981.1; PID:g5053
R;Bornheim, L.M.; Correia, M.A.
Mol. Pharmacol. 38, 319-326, 1990
A;Title: Selective inactivation of mouse liver cytochrome P-450IIIA by cannabidiol.
A;Reference number: A60564; MUID:90384441; PMID:2402224
A;Accession: A60564
A;Molecule type: protein
A;Residues: 1-17,'X',19-20,'X',22-24 <BOR>
C;Comment: This member of the cytochrome P450IIIA family was designated UT because it c
lation of testosterone.
C;Genetics:
A;Gene: Cyp3a11
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; heme; iron; metall
F;303-465/Domain: cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match            76.1%;  Score 1935.5;  DB 2;  Length 504;
  Best Local Similarity  73.1%;  Pred. No. 6.9e-137;
  Matches  351;  Conservative   64;  Mismatches   64;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62

Db         25 YGTRKHELFKKQGIPGPKPLPFLGTVLNYYKGLWKFDMECYKKYGKTWGLFDGQTPLLAV 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122

Db         85 TDPETIKNVLVKECFSVFTNRRDFGPVGIMSKAISISKDDEWKRYRALLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182

Db        145 MFPVIEQYGDILVKYLRQKAKKGKPVTMKDVLGAYSMDVITSTSFGVNVDSLNNPEDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242

Db        205 EKAKKLLRFDFFDPLLFSVVLFPFLTPVYEMLNICMFPKDSIEFFKKFVDRMKESRLDSK 264

Qy        243 QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301

Db        265 QKHRVDFLQLMMNSHNNSKDKVSHKALSDMEITAQSIIFIFAGYETTSSTLSFTLHSLAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361

Db        325 HPDIQKKLQDEIDEALPNKAPPTYDTVMEMEYLDMVLNETLRLYPIANRLERVCKKDVEL 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
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Db        385 NGVYIPKGSTVMIPSYALHHDPQHWSEPEEFQPERFSKENKGSIDPYVYLPFGNGPRNCL 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||||||||||| :::|||||:|||||||||||||  ||||||||:||||  ||  ::||
Db        445 GMRFALMNMKLALTKIMQNFSFQPCKETQIPLKLSRQGLLQPEKPIVLKVVPRDAVITGA 504


RESULT 14
A25222
cytochrome P450 3A2 - rat
N;Alternate names: cytochrome P450CN2, pregnenolone 16-alpha-carbonitrile-inducible; tes
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 09-Jul-2004
C;Accession: A25222; S27108; S46938; PX0032; PX0034; S30379
R;Gonzalez, F.J.; Song, B.J.; Hardwick, J.P.
Mol. Cell. Biol. 6, 2969-2976, 1986
A;Title: Pregnenolone 16-alpha-carbonitrile-inducible P-450 gene family: gene conversion
A;Reference number: A25222; MUID:87064606; PMID:3785219
A;Accession: A25222
A;Molecule type: mRNA
A;Residues: 1-504 <GON>
A;Cross-references: UNIPROT:P05183; GB:M13646; NID:g203827; PIDN:AAA41051.1; PID:g203828
A;Note: the authors translated the codon GAC for residue 445 as Gly
R;Telhada, M.B.; Pereira, T.M.; Lechner, M.C.
Arch. Biochem. Biophys. 298, 715-725, 1992
A;Title: Effect of dexamethasone and phenobarbital on run-on transcription rate and CYP3
A;Reference number: S27107; MUID:93037516; PMID:1417000
A;Accession: S27108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-36 <TEL>
A;Cross-references: EMBL:X62087
R;Miyata, M.; Nagata, K.; Shimada, M.; Yamazoe, Y.; Kato, R.
submitted to the EMBL Data Library, May 1994
A;Description: Structure of a gene and cDNA of a major constitutive form of testosterone
A;Reference number: S46938
A;Accession: S46938
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-428,'D',430-444,'G',446-504 <MIY>
A;Cross-references: EMBL:X79320; NID:g515381; PIDN:CAA55888.1; PID:g515382
R;Nagata, K.; Gonzalez, F.J.; Yamazoe, Y.; Kato, R.
J. Biochem. 107, 718-725, 1990
A;Title: Purification and characterization of four catalytically active testosterone 6be
nally related forms.
A;Reference number: PX0032; MUID:90375438; PMID:2398038
A;Accession: PX0032
A;Molecule type: protein
A;Residues: 1-21,'X',23-26,'X',28-29,'X',31-33 <NAG>
A;Experimental source: liver, Sprague-Dawley male rat
A;Accession: PX0034
A;Molecule type: protein
A;Residues: 1-27,'X',29,'X',31-33 <NA2>
R;Cooper, K.O.; Reik, L.M.; Jayyosi, Z.; Bandiera, S.; Kelley, M.; Ryan, D.E.; Daniel, R
Arch. Biochem. Biophys. 301, 345-354, 1993
A;Title: Regulation of two members of the steroid-inducible cytochrome P450 subfamily (3
A;Reference number: S30378; MUID:93213168; PMID:7681660
A;Accession: S30379
A;Molecule type: protein
A;Residues: 1-25 <COO>
C;Genetics:
A;Gene: CYP3A2
A;Introns: 24/2
A;Note: this list of introns is incomplete
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;303-465/Domain: cytochrome P450 homology <P45>
F;443/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             74.9%;  Score 1904.5;  DB 2;  Length 504;
  Best Local Similarity   72.2%;  Pred. No. 1.4e-134;
  Matches  346;  Conservative   68;  Mismatches   64;  Indels    1;  Gaps    1;

Qy          4 GTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAIT 63
              ||| ||:||| ||||| |||||| :|:|:||   |||||:|||||:|| :||| || ||
Db         26 GTHRHGIFKKQGIPGPKPLPFLGTVLNYYKGLGRFDMECYKKYGKIWGLFDGQTPVFAIM 85

Qy         64 DPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKEM 123
              | :||| ||||||:|||||| ||||| |  |:|:|:|||||| |:|||||||||:||||
Db         86 DTEMIKNVLVKECFSVFTNRRDFGPVGIMGKAVSVAKDEEWKRYRALLSPTFTSGRLKEM 145

Qy        124 VPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFVE 183
              ||| ||||:||: |::|||||||||:| |||||||||||||||||:||||||:|||||
Db        146 FPIIEQYGDILVKYLKQEAETGKPVTMKKVFGAYSMDVITSTSFGVNVDSLNNPKDPFVE 205

Qy        184 NTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDTQ 243
              ||||||||| || |||: :|||| || |:||||:||::   | :| | |:||:||:
Db        206 KTKKLLRFDFFDPLFLSVVLFPFLTPIYEMLNICMFPKDSIAFFQKFVHRIKETRLDSKH 265

Qy        244 KHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||:::  |||:  |||||||:|::|||:|||||||||||| |||::| ||||
Db        266 KHRVDFLQLMLNAHNNSKDEVSHKALSDVEIIAQSVIFIFAGYETTSSTLSFVLYFLATH 325

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||:|:|||||||  ||:|||||||:|::|||||||:||||||:||  |||||||||:|::
Db        326 PDIQKKLQEEIDGALPSKAPPTYDIVMEMEYLDMVLNETLRLYPIGNRLERVCKKDIELD 385

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
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Db        386 GLFIPKGSVVTIPTYALHHDPQHWPKPEEFHPERFSKENKGSIHPYVYLPFGNGPRNCID 445

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
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Db        446 MRFALMNMKLALTKVLQNFSFQPCKETQIPLKLSRQAILEPEKPIVLKVLPRDAVINGA 504


RESULT 15
JX0334
cytochrome P450 3A RL33 - rat
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: JX0334; S39797
R;Komori, M.; Oda, Y.
J. Biochem. 116, 114-120, 1994
A;Title: A major glucocorticoid-inducible P450 in rat liver is not P450 3A1.
A;Reference number: JX0334; MUID:95096005; PMID:7528203
A;Accession: JX0334
A;Molecule type: mRNA
A;Residues: 1-502 <KOM>
A;Cross-references: UNIPROT:Q06884; GB:D29967; NID:g479038; PIDN:BAA06233.1; PID:g479039
A;Experimental source: liver
R;Kirita, S.; Matsubara, T.
Arch. Biochem. Biophys. 307, 253-258, 1993
A;Title: cDNA cloning and characterization of a novel member of steroid-induced cytochro
A;Reference number: S39797; MUID:94099605; PMID:8274011
A;Accession: S39797
A;Molecule type: mRNA
A;Residues: 1-106,'D',108-502 <KIR>
A;Cross-references: EMBL:D13912; NID:g220835; PIDN:BAA03008.1; PID:g220836; GB:X96721; N
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metalloprotein; monooxygenase; oxidoreductase; tr
F;301-463/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             74.8%;  Score 1902.5;  DB 2;  Length 502;
  Best Local Similarity   72.5%;  Pred. No. 2e-134;
  Matches  348;  Conservative   64;  Mismatches   65;  Indels    3;  Gaps    2;

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Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
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Qy        183 ENTKKLLRFDPLDPFFLSITVFPPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242

Db        203 EKAKKLLRIDFFDPLFLSVVLFPPFLTPVYEMLNICMFPKDSIEFFKKFVYRMKETRLDSV 262

Qy        243 QKHRVDFLQLMIDSQN-SKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301

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Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421

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Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481

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Search completed: July 8, 2005, 14:14:16
Job time : 43 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: July 8, 2005, 14:14:33 ; Search time 166 Seconds
(without alignments)
1128.736 Million cell updates/sec

Title: US-10-690-991-2
Perfect score: 2542
Sequence: 1 MAYGTHSHGLFKKLGIPGPT.....PVVLKVESRDGTVSGAHHHH 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2542	100.0	485	16	US-10-690-991-2	Sequence 2, Appli
2	2542	100.0	485	17	US-10-833-296-2	Sequence 2, Appli
3	2501	98.4	503	15	US-10-313-963A-56	Sequence 56, Appl
4	2494	98.1	503	14	US-10-146-575-2	Sequence 2, Appli
5	2449.5	96.4	504	16	US-10-804-772-24	Sequence 24, Appl
6	2372	93.3	503	17	US-10-732-923-1079	Sequence 1079, Ap
7	2233	87.8	503	9	US-09-957-997-3	Sequence 3, Appli
8	2011.5	79.1	499	17	US-10-626-686-66	Sequence 66, Appl
9	1958	77.0	502	14	US-10-274-694-7	Sequence 7, Appli
10	1958	77.0	502	16	US-10-332-448-7	Sequence 7, Appli
11	1957	77.0	503	13	US-10-007-814-2	Sequence 2, Appli
12	1956	76.9	503	15	US-10-112-944-432	Sequence 432, App
13	1946.5	76.6	504	13	US-10-007-814-4	Sequence 4, Appli
14	1882	74.0	508	14	US-10-274-694-16	Sequence 16, Appl
15	1882	74.0	508	16	US-10-332-448-16	Sequence 16, Appl
16	1620	63.7	420	13	US-10-007-814-6	Sequence 6, Appli
17	905	35.6	217	14	US-10-106-698-6001	Sequence 6001, Ap
18	840.5	33.1	534	13	US-10-087-192-2004	Sequence 2004, Ap
19	840.5	33.1	534	16	US-10-741-601-291	Sequence 291, App
20	840.5	33.1	534	16	US-10-741-601-292	Sequence 292, App
21	832.5	32.7	515	17	US-10-732-923-1068	Sequence 1068, Ap
22	824.5	32.4	543	13	US-10-087-192-2001	Sequence 2001, Ap
23	802	31.5	250	13	US-10-007-814-8	Sequence 8, Appli
24	678.5	26.7	518	17	US-10-732-923-1069	Sequence 1069, Ap
25	668.5	26.3	496	9	US-09-945-301-4	Sequence 4, Appli
26	668.5	26.3	496	14	US-10-067-668-10	Sequence 10, Appl
27	668.5	26.3	496	14	US-10-175-696-10	Sequence 10, Appl
28	668.5	26.3	496	16	US-10-776-871-10	Sequence 10, Appl
29	668.5	26.3	496	16	US-10-782-695-19	Sequence 19, Appl
30	659.5	25.9	445	14	US-10-032-189-73	Sequence 73, Appl
31	659.5	25.9	445	15	US-10-072-012-848	Sequence 848, App
32	658.5	25.9	440	15	US-10-074-978A-209	Sequence 209, App
33	658.5	25.9	460	16	US-10-741-601-293	Sequence 293, App
34	631	24.8	470	14	US-10-067-668-12	Sequence 12, Appl
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37	623	24.5	520	15	US-10-369-493-5530	Sequence 5530, Ap
38	620.5	24.4	519	15	US-10-369-493-5529	Sequence 5529, Ap
39	610.5	24.0	423	15	US-10-231-913-274	Sequence 274, App
40	594	23.4	520	15	US-10-369-493-5531	Sequence 5531, Ap
41	591.5	23.3	518	15	US-10-369-493-5532	Sequence 5532, Ap
42	590.5	23.2	510	14	US-10-021-425-36	Sequence 36, Appl
43	590.5	23.2	510	15	US-10-369-493-5677	Sequence 5677, Ap
44	590.5	23.2	510	17	US-10-900-856-39	Sequence 39, Appl
45	588.5	23.2	522	15	US-10-369-493-5678	Sequence 5678, Ap

ALIGNMENTS

RESULT 1
US-10-690-991-2
; Sequence 2, Application US/10690991
; Publication No. US20040243319A1
; GENERAL INFORMATION:
; APPLICANT: Tickle, Ian J
; APPLICANT: Vonrhein, Clemens
; APPLICANT: Williams, Pamela A
; APPLICANT: Jhoti, Harren
; APPLICANT: Kirton, Stewart Brian
; TITLE OF INVENTION: Crystal structure of cytochrome P450
; FILE REFERENCE: 620-282
; CURRENT APPLICATION NUMBER: US/10/690,991
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: US 60/421,063
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GB02/02668
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 10/221,036
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US 60/479,448
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region to
; OTHER INFORMATION: delete the hydrophobic trans-membrane domain, and the region
; OTHER INFORMATION: replaced by a short N-terminal sequence.
US-10-690-991-2

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  Query Match           100.0%;  Score 2542;  DB 16;  Length 485;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-218;
  Matches  485;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60
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Db          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60

Qy         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120

Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
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Db        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180

Qy        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240
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Qy        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300
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Db        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300

Qy        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360
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Db        301 THPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVE 360

Qy        361 INGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNC 420
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Qy        421 IGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
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Qy        481 AHHHH 485
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Db        481 AHHHH 485


RESULT 2
US-10-833-296-2
; Sequence 2, Application US/10833296
; Publication No. US20050032119A1
; GENERAL INFORMATION:
;  APPLICANT: Tickle, Ian J
;  APPLICANT:  Vonrhein, Clemens
;  APPLICANT:  Vinkovic, Dijana M
;  APPLICANT:  Kirton, Stewart
;  APPLICANT:  Williams, Pamela A
;  APPLICANT:  Jhoti, Harren
;  TITLE OF INVENTION: Crystal Structure of Cytochrome P450
;  FILE REFERENCE: 620-305
;  CURRENT APPLICATION NUMBER: US/10/833,296
;  CURRENT FILING DATE:  2004-04-28
;  PRIOR APPLICATION NUMBER: GB 0108214.8
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: GB 0108212.2
;  PRIOR FILING DATE: 2001-04-02
;  PRIOR APPLICATION NUMBER: US 60/479,448
;  PRIOR FILING DATE: 2003-06-19
;  PRIOR APPLICATION NUMBER: US 60/421,063
;  PRIOR FILING DATE: 2002-10-25
;  PRIOR APPLICATION NUMBER: US 60/306,873
;  PRIOR FILING DATE: 2001-07-23
;  PRIOR APPLICATION NUMBER: US 60/306,874
;  PRIOR FILING DATE: 2001-07-23
;  PRIOR APPLICATION NUMBER: US 10/690,991
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/221,036
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: PCT/GB02/02668
;  PRIOR FILING DATE: 2002-05-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 485
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Human 3A4 P450 protein truncated in its N-terminal region
;   OTHER INFORMATION: to delete the hydrophobic trans-membrane domain, and the
;   OTHER INFORMATION: region replaced by a short N-terminal sequence.
US-10-833-296-2

  Query Match           100.0%;  Score 2542;  DB 17;  Length 485;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-218;
  Matches  485;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60
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Db          1 MAYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVL 60

Qy         61 AITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKL 120
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Qy        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180
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Db        121 KEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDP 180

Qy        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240
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Db        181 FVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLE 240

Qy        241 DTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELA 300
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RESULT 3
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; Sequence 56, Application US/10313963A
; Publication No. US20040002078A1
; GENERAL INFORMATION:
;  APPLICANT: Boutell, Jonathan
;  APPLICANT:  Godber, Benjamin
;  APPLICANT:  Hart, Darren
;  APPLICANT:  Blackburn, Jonathan
;  TITLE OF INVENTION: Arrays
;  FILE REFERENCE: KIL-001
;  CURRENT APPLICATION NUMBER: US/10/313,963A
;  CURRENT FILING DATE:  2003-06-19
;  PRIOR APPLICATION NUMBER: US 60/335,806
;  PRIOR FILING DATE: 2001-12-05
;  PRIOR APPLICATION NUMBER: US 60/410,815
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 56
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-313-963A-56

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  Matches  479;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 4
US-10-146-575-2
; Sequence 2, Application US/10146575
; Publication No. US20030059800A1
; GENERAL INFORMATION:
;  APPLICANT: Lichter, Jay
;  APPLICANT:  Guido, Marco
;  TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
;  FILE REFERENCE: SEQ-12P
;  CURRENT APPLICATION NUMBER: US/10/146,575
;  CURRENT FILING DATE:  2002-05-14
;  PRIOR APPLICATION NUMBER: US/09/144,367
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 58
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: H. sapiens
US-10-146-575-2

  Query Match            98.1%;  Score 2494;  DB 14;  Length 503;
  Best Local Similarity  99.8%;  Pred. No. 7.4e-214;
  Matches  478;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 503


RESULT 5
US-10-804-772-24
; Sequence 24, Application US/10804772
; Publication No. US20040244077A1
; GENERAL INFORMATION:
;  APPLICANT: Azpiroz, Ricardo
;  APPLICANT:  Choe, Sunghwa
;  APPLICANT:  Feldmann, Kenneth A.
;  TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
;  FILE REFERENCE: 11696-070001
;  CURRENT APPLICATION NUMBER: US/10/804,772
;  CURRENT FILING DATE:  2004-03-18
;  PRIOR APPLICATION NUMBER: US/09/502,426
;  PRIOR FILING DATE: 2000-02-11
;  PRIOR APPLICATION NUMBER: US 60/119,657
;  PRIOR FILING DATE: 1999-02-11
;  PRIOR APPLICATION NUMBER: US 60/119,658
;  PRIOR FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24
;   LENGTH: 504
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-804-772-24

  Query Match            96.4%;  Score 2449.5;  DB 16;  Length 504;
  Best Local Similarity  97.9%;  Pred. No. 7e-210;
  Matches  470;  Conservative    4;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              ||||||| |||||||||||||| |||||||||||||||||||||||||||||||||||||
Db         85 TDPDMIKLVLVKECYSVFTNREPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||| |||||||||||||||||||:|||||:||||||||| |
Db        145 MVPIIAQYGDVLVRNLRRERETGKPVTLKDVFGAYSMDVITSSSFGVNVDSLNNPQDPLV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        205 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKAVKRMKESRLEDT 264
```

```
Qy        243 QKHRVDFLQLMIDS-QNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              |||||||||||||| :|||||||||||||||||||||||||||||||||||||||||||||
Db        265 QKHRVDFLQLMIDSHKNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 324

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 384

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 NGMFIPKGWVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 504
```

RESULT 6
US-10-732-923-1079
; Sequence 1079, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1079
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-732-923-1079

Query Match 93.3%; Score 2372; DB 17; Length 503;
Best Local Similarity 93.9%; Pred. No. 5.9e-203;
Matches 450; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||| ||||||| ||| |||||:||||||||||||:||||||
Db         25 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGFWTFDMECYKKYGKVWGFYDGRQPVLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:|||||||||||||||||||||||:|||||||||||:||||||||||||||||||||
Db         85 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||:|||:|||||||| :||||||:||||||||:|||||:||
Db        205 ENTKKLLRFDFLDPFFLSITIFPFIIPILEVLNISIFPREVTSFLRKSVKRIKESRLKDT 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||
Db        265 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||| ||||||||||||||||||||||||||:||||||||||||||||||
Db        325 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMVVNETLRIFPIAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||||||||||||| ||||| |||||||||||||| ||||||||||||||||||||
Db        385 GIFIPKGVVVMIPSYALHHDPKYWPEPEKFLPERFSKKNNDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||:|||||||||||||||||||| |||||| |||:|||:||||||||||
Db        445 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 503
```

RESULT 7
US-09-957-997-3
; Sequence 3, Application US/09957997
; Patent No. US20020150915A1
; GENERAL INFORMATION:
; APPLICANT: Berkenstam, Anders
; APPLICANT: Bertilsson, Gran
; APPLICANT: Blomquist, Patrik
; TITLE OF INVENTION: PROMOTER SEQUENCES
; FILE REFERENCE: 13425-046001
; CURRENT APPLICATION NUMBER: US/09/957,997
; CURRENT FILING DATE: 2001-09-21
; EARLIER APPLICATION NUMBER: SE 0003393-6
; EARLIER FILING DATE: 2000-09-22
; EARLIER APPLICATION NUMBER: 60/238,895
; EARLIER FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-957-997-3

Query Match 87.8%; Score 2233; DB 9; Length 503;
Best Local Similarity 88.7%; Pred. No. 1.6e-190;
Matches 425; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

```
Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              ||| :|||||||||||||||||| ||: ||:  |||||:||| |||| || |||:|||
Db         25 YGTRTHGLFKKLGIPGPTPLPFLGNALSFRKGYWTFDMECYKKYRKVWGIYDCQQPMLAI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||||||||||||||||:|||||||||||:|||||||||||||||||
Db         85 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||||||||||||||||||||||||||| ||||||||||||||||:||||||||||||
Db        145 MVPIIAQYGDVLVRNLRREAETGKPVTLKHVFGAYSMDVITSTSFGVSIDSLNNPQDPFV 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              |||||||||: |||| ||| ||||| |||| ||| ||||:| :|| ||||::|| ||::|
Db        205 ENTKKLLRFNPLDPFVLSIKVFPFLTPILEALNITVFPRKVISFLTKSVKQIKEGRLKET 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              |||||||||||||||||::|:|||||||||:|||||||||||||||||||||:||||||
Db        265 QKHRVDFLQLMIDSQNSKDSETHKALSDLELMAQSIIFIFAGYETTSSVLSFIIYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              ||||||:|:||| |||||||||||||:|||||||||||||:||||||||||||||||||
Db        325 PDVQQKVQKEIDTVLPNKAPPTYDTVLQLEYLDMVVNETLRLFPVAMRLERVCKKDVEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |||||||||||||| || |||||||||||||||||||||||||||||||||||||||||||
Db        385 GMFIPKGVVVMIPSYVLHHDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              |||||:||||||:|||||||||||||||||||  ||||  |||:||| |||| |||||
Db        445 MRFALVNMKLALVRVLQNFSFKPCKETQIPLKLRFGGLLLTEKPIVLKAESRDETVSGA 503
```

RESULT 8
US-10-626-686-66
; Sequence 66, Application US/10626686
; Publication No. US20050074842A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Kimura, Tomoko
; TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
; TITLE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PROTEINS
; FILE REFERENCE: GIN-6706CPUS

```
;  CURRENT APPLICATION NUMBER: US/10/626,686
;  CURRENT FILING DATE:  2003-07-25
;  PRIOR APPLICATION NUMBER: US/09/445,258A
;  PRIOR FILING DATE: 1999-12-01
;  PRIOR APPLICATION NUMBER: PCT/US98/02445
;  PRIOR FILING DATE: 1998-06-03
;  PRIOR APPLICATION NUMBER: JP 9-144948
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
;   LENGTH: 499
;   TYPE: PRT
;   ORGANISM: Macaca fascicularis
US-10-626-686-66

  Query Match             79.1%;  Score 2011.5;  DB 17;  Length 499;
  Best Local Similarity   82.0%;  Pred. No. 9.7e-171;
  Matches  393;  Conservative   16;  Mismatches    9;  Indels   61;  Gaps    2;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||||||||||||||||| ||||||| |||   ||||:|||||||||||:||||||
Db         82 YGTHSHGLFKKLGIPGPTPLPLLGNILSYRKGF-WTDMECYKKYGKVWGFYDGRQPVLAI 140

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||:||||||||||||||||||||||:||||||||||:||||||||||||||||||||
Db        141 TDPNMIKTVLVKECYSVFTNRRPFGPVGFMKNAISIAEDEEWKRIRSLLSPTFTSGKLKE 200

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              ||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 MVPIIAKYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 260

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              ||||||||||||||||||:|||:|||||||||| :||||||:|||||||:|||||:||
Db        261 ENTKKLLRFDFLDPFFLSITIFPFIIPILEVLNISIFPPREVTSFLRKSVKRIKESRLKDT 320

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db        321 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIIYELATH 380

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||| ||||||||||||||||||||
Db        381 PDVQQKLQEEIDTVLPNKAPPTYDTVLQMEYLDMV---------------------------- 415

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
                                                |||| ||||||||||||||||||||
Db        416 -----------------------------------SKKNNDNIDPYIYTPFGSGPRNCIG 440

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSGA 481
              ||||||||||:||||||||||||||||||||| |||||| |||:|||:||||||||||
Db        441 MRFALMNMKLAIIRVLQNFSFKPCKETQIPLKLRLGGLLQTEKPIVLKIESRDGTVSGA 499


RESULT 9
US-10-274-694-7
; Sequence 7, Application US/10274694
; Publication No. US20030143589A1
; GENERAL INFORMATION:
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT:  BRUNS, Christopher M.
;  APPLICANT:  DAS, Debopriya
;  APPLICANT:  DING, Li
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  LEE, Ernestine A.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  LU, Yan
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  PATTERSON, Chandra S.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  RING, Huijun Z.
;  APPLICANT:  SANJANWALA, Madhusudan M.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  THORNTON, Michael B.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  WALIA, Narinder K.
;  APPLICANT:  XU, Yuming
;  APPLICANT:  YANG, Junming
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  YUE, Henry
;  TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
;  FILE REFERENCE: PI-0151 USA
;  CURRENT APPLICATION NUMBER: US/10/274,694
;  CURRENT FILING DATE:  2002-10-18
;  PRIOR APPLICATION NUMBER: 60/221,837
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/220,037
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 60/218,948
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/21324
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/216,804
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030143589A1 7476298CD1
US-10-274-694-7

  Query Match             77.0%;  Score 1958;  DB 14;  Length 502;
  Best Local Similarity   76.0%;  Pred. No. 5.9e-166;
  Matches  364;  Conservative   52;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          2 AYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLA 61
              :||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:|
Db         23 SYGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLV 82

Qy         62 ITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLK 121
              | |||||||||||||||||: | ||:||:|||:| ||||||||:|:|||| ||| | |
Db         83 IMDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFK 142

Qy        122 EMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPF 181
              ||||||:|||:|||:||:|||  | : ||| ||||:|||||| | ||||:||||||||||
Db        143 EMVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPF 202

Qy        182 VENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLED 241
              ::| |||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        203 LKNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKD 262

Qy        242 TQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              ||||||| | ||||||||||:||||||||||||||| ||| |:|||: | ||||||||
Db        263 KQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELAT 322

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              |||||||||||||||||||| ||| ::|||||||||||||||:  |: |||||||:||
Db        323 HPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEI 382

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              ||:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:||||||
Db        383 NGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCI 442

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||| |:|||:|| ||||||||||||||||    :||||||:||||  |||  ||
Db        443 GMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 501
```

```
RESULT 10
US-10-332-448-7
; Sequence 7, Application US/10332448
; Publication No. US20040253588A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
;  APPLICANT:  BRUNS, Christopher M.; DAS, Debopriya Das;
;  APPLICANT:  DING, Li; ELLIOTT, Vicki S.; GANDHI, Ameena R.;
;  APPLICANT:  HAFALIA, April; KEARNEY, Liam; KHAN, Farrah A.;
;  APPLICANT:  LAL, Preeti; LEE, Ernestine A.; LU, Dyung Aina M.;
;  APPLICANT:  LU, Yan; DANNIEL, Nguyen B.; ARVIZU, Chandra S.;
;  APPLICANT:  RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
;  APPLICANT:  SANJANWALA, Madhu S.; TANG, Y. Tom;
;  APPLICANT:  THANGAVELU, Kavitha; THORNTON, Michael;
;  APPLICANT:  TRIBOULEY, Catherine M.; WALIA, Narinder K.;
;  APPLICANT:  XU, Yuming; YANG, Junming; YAO, Monique G.; YUE, Henry
;  TITLE OF INVENTION: Drug Metabolizing Enzymes
;  FILE REFERENCE: PI-0151 USN
;  CURRENT APPLICATION NUMBER: US/10/332,448
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: US 60/216,804
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/218,948
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/220,037
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/221,837
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: 502
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7476298CD1
US-10-332-448-7

  Query Match             77.0%;  Score 1958;  DB 16;  Length 502;
  Best Local Similarity   76.0%;  Pred. No. 5.9e-166;
  Matches  364;  Conservative   52;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          2 AYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLA 61
              :|||||| |||||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         23 SYGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLV 82

Qy         62 ITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLK 121
              | |||||||||||||||||||: | ||:||:|||:| |||||||||:|:|||| ||| | |
Db         83 IMDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFK 142

Qy        122 EMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPF 181
              ||||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:|||||||||
Db        143 EMVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPF 202

Qy        182 VENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLED 241
              ::| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        203 LKNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKD 262

Qy        242 TQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELAT 301
              ||||||| | |||||||||:|||||||||||||||| ||| |:|||: | ||||||||
Db        263 KQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELAT 322

Qy        302 HPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEI 361
              |||||||||||||||||||| ||| ::|||||||||||||||:  |: ||||||:||
Db        323 HPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEI 382

Qy        362 NGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCI 421
              ||:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:||||||
Db        383 NGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCI 442

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||| |:|||:|| |||||||||||||||||    :||||||:|||| |||  ||
Db        443 GMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 501


RESULT 11
US-10-007-814-2
; Sequence 2, Application US/10007814
; Publication No. US20020160479A1
; GENERAL INFORMATION:
;  APPLICANT: Wojnowski, Leszek
;  APPLICANT:  Gellner, Klaus
;  APPLICANT:  Eiselt, Regina
;  TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
;  TITLE OF INVENTION:  (CYP3A) GENE FAMILY: CYP3AX
;  FILE REFERENCE: 310115.401D1
;  CURRENT APPLICATION NUMBER: US/10/007,814
;  CURRENT FILING DATE:  2001-11-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-814-2

  Query Match             77.0%;  Score 1957;  DB 13;  Length 503;
  Best Local Similarity   76.2%;  Pred. No. 7.3e-166;
  Matches  364;  Conservative   51;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||||: | ||:||:|||:| |||||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | |||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||||| ||| ::|||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:|||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||| |:|||:|| |||||||||||||||||    :||||||:|||| |||  ||
Db        445 MRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 502


RESULT 12
US-10-112-944-432
; Sequence 432, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
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;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Zhiwei
;  TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
;  TITLE OF INVENTION:  Secreted Polypeptides
;  FILE REFERENCE: 805A
;  CURRENT APPLICATION NUMBER: US/10/112,944
;  CURRENT FILING DATE:  2002-03-28
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  NUMBER OF SEQ ID NOS: 924
;  SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 432
;   LENGTH: 503
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-112-944-432

  Query Match             76.9%;  Score 1956;  DB 15;  Length 503;
  Best Local Similarity   76.2%;  Pred. No. 8.9e-166;
  Matches  364;  Conservative   50;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||: | ||:||:|||:| |||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| ||||: |||||| | | :|||| |: | ||| :|||:||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLIALFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | ||||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||||| ||| ::|||||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGSGPRNCIG 422
              |:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:|||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGAGPRNCIG 444

Qy        423 MRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              ||||| |:|||:|| ||||||||||||||||||    :||||||:|||  |||  ||
Db        445 MRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 502


RESULT 13
US-10-007-814-4
; Sequence 4, Application US/10007814
; Publication No. US20020160479A1
; GENERAL INFORMATION:
;  APPLICANT: Wojnowski, Leszek
;  APPLICANT:  Gellner, Klaus
;  APPLICANT:  Eiselt, Regina
;  TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
;  TITLE OF INVENTION:  (CYP3A) GENE FAMILY: CYP3AX
;  FILE REFERENCE: 310115.401D1
;  CURRENT APPLICATION NUMBER: US/10/007,814
;  CURRENT FILING DATE:  2001-11-09
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 504
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-007-814-4

  Query Match             76.6%;  Score 1946.5;  DB 13;  Length 504;
  Best Local Similarity   76.0%;  Pred. No. 6.3e-165;
  Matches  364;  Conservative   51;  Mismatches   63;  Indels    1;  Gaps    1;

Qy          3 YGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMFDMECHKKYGKVWGFYDGQQPVLAI 62
              |||||| |||||||||||||||| || | :|   || ||::|||::|| |:||||:| |
Db         25 YGTHSHKLFKKLGIPGPTPLPFLGTILFYLRGLWNFDRECNEKYGEMWGLYEGQQPMLVI 84

Qy         63 TDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTFTSGKLKE 122
              |||||||||||||||||||: | ||:||:|||:| |||||||:|:|||| ||| | ||
Db         85 MDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAFTSVKFKE 144

Qy        123 MVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLNNPQDPFV 182
              |||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||||||||:
Db        145 MVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLNNPQDPFL 204

Qy        183 ENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMKESRLEDT 242
              :| ||||: |||||| | |::|||| |: | ||| :|||:||:||: |::|||||||:|
Db        205 KNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMKESRLKDK 264

Qy        243 QKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFIMYELATH 302
              ||||||| | ||||||||||:|||||||||||||||| ||| |:|||: | |||||||||
Db        265 QKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFIMYELATH 324

Qy        303 PDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEIN 362
              |||||||||||||||||||| ||| ::|||||||||||||||||:  |: ||||||:|||
Db        325 PDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVCKKDIEIN 384

Qy        363 GMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPE-RFSKKNKDNIDPYIYTPFGSGPRNCI 421
              |:|||||: ||:| |||| |||||||||| || ||||||||:|| | | |||:||||||
Db        385 GVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPESRFSKKNKDSIDLYRYIPFGAGPRNCI 444

Qy        422 GMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRDGTVSG 480
              |||||| |:|||:|| ||||||||||||||||||    :||||||:|||  |||  ||
Db        445 GMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRDGITSG 503


RESULT 14
US-10-274-694-16
; Sequence 16, Application US/10274694
; Publication No. US20030143589A1
; GENERAL INFORMATION:
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT:  BRUNS, Christopher M.
;  APPLICANT:  DAS, Debopriya
;  APPLICANT:  DING, Li
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  LEE, Ernestine A.
```

```
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  LU, Yan
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  PATTERSON, Chandra S.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  RING, Huijun Z.
;  APPLICANT:  SANJANWALA, Madhusudan M.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  THORNTON, Michael B.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  WALIA, Narinder K.
;  APPLICANT:  XU, Yuming
;  APPLICANT:  YANG, Junming
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  YUE, Henry
;  TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
;  FILE REFERENCE: PI-0151 USA
;  CURRENT APPLICATION NUMBER: US/10/274,694
;  CURRENT FILING DATE:  2002-10-18
;  PRIOR APPLICATION NUMBER: 60/221,837
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/220,037
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 60/218,948
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US01/21324
;  PRIOR FILING DATE: 2001-07-05
;  PRIOR APPLICATION NUMBER: 60/216,804
;  PRIOR FILING DATE: 2000-07-07
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PERL Program
; SEQ ID NO 16
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030143589A1 7478053CD1
US-10-274-694-16

  Query Match             74.0%;  Score 1882;  DB 14;  Length 508;
  Best Local Similarity   73.6%;  Pred. No. 3.7e-159;
  Matches  357;  Conservative   54;  Mismatches   68;  Indels    6;  Gaps    2;

Qy          2 AYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMF-DMECHKKYGKVWG-----FYDG 55
              :|||||| |||||||||||||||||| || | :    : :|: |:|  ::        |:|
Db         23 SYGTHSHKLFKKLGIPGPTPLPFLGTILFYLRVKTTYAEMKTHQKDNELLSVHRQKLYEG 82

Qy         56 QQPVLAITDPDMIKTVLVKECYSVFTNRRPFGPVGFMKSAISIAEDEEWKRLRSLLSPTF 115
              |||:| | |||||||||||||||||||: | ||:||:|||:| |||||||||:|:|||| |
Db         83 QQPMLVIMDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAF 142

Qy        116 TSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLN 175
              || | |||||||:| ||:|||:||:|||  | : ||| ||||:||||| | ||||:||||
Db        143 TSVKFKEMVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLN 202

Qy        176 NPQDPFVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMK 235
              ||||||:| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||
Db        203 NPQDPFLKNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMK 262

Qy        236 ESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFI 295
              ||||:| ||||||| | |||||||||||:|||||||||||||||| ||| |:|||: | ||
Db        263 ESRLKDKQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFI 322

Qy        296 MYELATHPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVC 355
              ||||||||||||||||||||||||||| ||| ::||||||||||||||||:  |: |||
Db        323 MYELATHPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVC 382

Qy        356 KKDVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGS 415
              |||:||||:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:
Db        383 KKDIEINGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGA 442

Qy        416 GPRNCIGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRD 475
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Db        503 GITSG 507


RESULT 15
US-10-332-448-16
; Sequence 16, Application US/10332448
; Publication No. US20040253588A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;
;  APPLICANT:  BRUNS, Christopher M.; DAS, Debopriya Das;
;  APPLICANT:  DING, Li; ELLIOTT, Vicki S.; GANDHI, Ameena R.;
;  APPLICANT:  HAFALIA, April; KEARNEY, Liam; KHAN, Farrah A.;
;  APPLICANT:  LAL, Preeti; LEE, Ernestine A.; LU, Dyung Aina M.;
;  APPLICANT:  LU, Yan; DANNIEL, Nguyen B.; ARVIZU, Chandra S.;
;  APPLICANT:  RAMKUMAR, Jayalaxmi; RING, Huijun Z.;
;  APPLICANT:  SANJANWALA, Madhu S.; TANG, Y. Tom;
;  APPLICANT:  THANGAVELU, Kavitha; THORNTON, Michael;
;  APPLICANT:  TRIBOULEY, Catherine M.; WALIA, Narinder K.;
;  APPLICANT:  XU, Yuming; YANG, Junming; YAO, Monique G.; YUE, Henry
;  TITLE OF INVENTION: Drug Metabolizing Enzymes
;  FILE REFERENCE: PI-0151 USN
;  CURRENT APPLICATION NUMBER: US/10/332,448
;  CURRENT FILING DATE:  2003-01-07
;  PRIOR APPLICATION NUMBER: US 60/216,804
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: US 60/218,948
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 60/220,037
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: US 60/221,837
;  PRIOR FILING DATE: 2000-07-28
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PERL Program
; SEQ ID NO 16
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7478053CD1
US-10-332-448-16

  Query Match             74.0%;  Score 1882;  DB 16;  Length 508;
  Best Local Similarity   73.6%;  Pred. No. 3.7e-159;
  Matches  357;  Conservative   54;  Mismatches   68;  Indels    6;  Gaps    2;

Qy          2 AYGTHSHGLFKKLGIPGPTPLPFLGNILSYHKGFCMF-DMECHKKYGKVWG-----FYDG 55
              :|||||| |||||||||||||||||| || | :    : :|: |:|  ::        |:|
Db         23 SYGTHSHKLFKKLGIPGPTPLPFLGTILFYLRVKTTYAEMKTHQKDNELLSVHRQKLYEG 82

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              |||:| | |||||||||||||||||||: | ||:||:|||:| |||||||||:|:|||| |
Db         83 QQPMLVIMDPDMIKTVLVKECYSVFTNQMPLGPMGFLKSALSFAEDEEWKRIRTLLSPAF 142

Qy        116 TSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTLKDVFGAYSMDVITSTSFGVNIDSLN 175
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Db        143 TSVKFKEMVPIISQCGDMLVRSLRQEAENSKSINLKDFFGAYTMDVITGTLFGVNLDSLN 202

Qy        176 NPQDPFVENTKKLLRFDFLDPFFLSITVFPFLIPILEVLNICVFPREVTNFLRKSVKRMK 235
              ||||||:| ||||: |||||| | |::|||| |: | ||| :||::||:||: |::|||
Db        203 NPQDPFLKNMKKLLKLDFLDPFLLLISLFPFLTPVFEALNIGLFPKDVTHFLKNSIERMK 262

Qy        236 ESRLEDTQKHRVDFLQLMIDSQNSKETESHKALSDLELVAQSIIFIFAGYETTSSVLSFI 295
              ||||:| ||||||| | |||||||||||:|||||||||||||||| ||| |:|||: | ||
Db        263 ESRLKDKQKHRVDFFQQMIDSQNSKETKSHKALSDLELVAQSIIIIFAAYDTTSTTLPFI 322

Qy        296 MYELATHPDVQQKLQEEIDAVLPNKAPPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVC 355
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                ||||||||||||||||||||||||||| ||| ::|||||||||||||||||:  |: |||
Db        323 MYELATHPDVQQKLQEEIDAVLPNKAPVTYDALVQMEYLDMVVNETLRLFPVVSRVTRVC 382

Qy        356 KKDVEINGMFIPKGVVVMIPSYALHRDPKYWTEPEKFLPERFSKKNKDNIDPYIYTPFGS 415
                |||:||||:|||||: ||:| |||| |||||||||| ||||||||||:|| | | |||:
Db        383 KKDIEINGVFIPKGLAVMVPIYALHHDPKYWTEPEKFCPERFSKKNKDSIDLYRYIPFGA 442

Qy        416 GPRNCIGMRFALMNMKLALIRVLQNFSFKPCKETQIPLKLSLGGLLQPEKPVVLKVESRD 475
                |||||||||||  |:|||:|| |||||||||||||||||    :||||||:||||  ||
Db        443 GPRNCIGMRFALTNIKLAVIRALQNFSFKPCKETQIPLKLDNLPILQPEKPIVLKVHLRD 502

Qy        476 GTVSG 480
                |  ||
Db        503 GITSG 507


Search completed: July  8, 2005, 14:30:06
Job time : 170 secs
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